

183386

STIC-Biotech/ChemLib

From: Mertz, Prema
Sent: Monday, March 27, 2006 4:08 PM
To: STIC-Biotech/ChemLib
Subject: 10/849,979

Please search any 6 amino acids of SEQ ID NO:139 with protein databases.

Thanks.

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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 8
Searcher Prep Time: _____
Online Time: 8
Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
CM 1646 Tel: 308-4491
3-30
3-30

Type of Search
NA# _____ AA# 1
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 09:04:17 ; Search time 188 Seconds
(without alignments)
1187,258 Million cell updates/sec

Title: US-10-849-979-139

Perfect score: 508
Sequence: 1 MDRKLGMAASLAVALLL.....NYIEGTYLFAAFLEMAQLH 508

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 6

Total number of hits satisfying chosen parameters: 38162

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980b.*
2: geneseqp1990a.*
3: geneseqp2000a.*
4: geneseqp2001a.*
5: geneseqp2002a.*
6: geneseqp2003a.*
7: geneseqp2003ba.*
8: geneseqp2004a.*
9: geneseqp2005a.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	508	4 AAB97262	AAB97262 Human cat
2	508	100.0	508	4 AAG89122	AAG89122 Human sec
3	508	100.0	508	6 ABR47759	ABR47759 Human sec
4	508	100.0	508	6 ABR00082	ABR00082 Human gen
5	508	100.0	508	7 ABR91551	ABR91551 Human sec
6	508	100.0	508	7 ADC74152	ADC74152 Human sec
7	508	100.0	508	7 ADE11767	ADE11767 Human sec
8	508	100.0	509	3 AAY76144	AAY76144 Human sec
9	492	96.9	507	5 AAU72908	AAU72908 Human met
10	492	96.9	507	5 ABB07950	ABB07950 Human met
11	492	96.9	507	6 ABO69115	ABO69115 Human PRO
12	492	96.9	507	6 ABO19431	ABO19431 Human sec
13	492	96.9	507	6 ABU69092	ABU69092 Human PRO
14	492	96.9	507	6 ABU81556	ABU81556 Human sec
15	492	96.9	507	6 ADA76582	ADA76582 Novel hum
16	492	96.9	507	7 ABO25139	ABO25139 Human sec
17	492	96.9	507	7 AAE39109	AAE39109 Human PRO
18	492	96.9	507	7 AAE39046	AAE39046 Human PRO
19	492	96.9	507	7 ADC29813	ADC29813 Novel hum
20	492	96.9	507	8 ADP09256	ADP09256 Human sec
21	492	96.9	507	9 ADW12488	ADW12488 Human PRO
22	492	96.9	507	9 AEB45360	AEB45360 Human W11
23	429	84.4	501	4 AAU28396	AAU28396 Human act
24	429	84.4	501	4 AAU25426	AAU25426 Human Sch

25	429	84.4	501	4 AAU5115	AAU5115 Schizophr
26	429	84.4	501	8 ADO79056	ADO79056 Schizophr
27	391	77.0	507	3 AAB18921	AAB18921 A novel P
28	336	66.1	342	4 AAM40149	AAM40149 Human pol
29	326	64.2	358	4 AAM41935	AAM41935 Human pol
30	235	46.3	508	7 ADC77691	ADC77691 Human 550
31	178	35.0	498	4 AAU26543	AAU26543 Protein e
32	148	29.1	171	8 ADO67596	ADO67596 Novel hum
33	126	24.8	133	4 AAM25912	AAM25912 Human pro
34	119	23.4	119	4 AAM24283	AAM24283 Human EST
35	100	19.7	316	5 ABB89681	ABB89681 Human pol
36	54	10.6	100	4 ABO1654	ABO1654 Novel hum
37	41	8.1	41	9 AEB45362	AEB45362 Fragment
38	37	7.3	157	4 ABO1653	ABO1653 Novel hum
39	26	5.1	42	9 AEB45364	AEB45364 Fragment
40	15	3.0	15	4 AAU28401	AAU28401 Tryptic d
41	15	3.0	15	4 AAU24970	AAU24970 Schizophr
42	15	3.0	15	4 AAU26540	AAU26540 Tryptic d
43	15	3.0	15	4 AAU15314	AAU15314 Schizophr
44	15	3.0	15	8 ADO78581	ADO78581 Schizophr
45	15	3.0	15	8 ADO79039	ADO79039 Schizophr
46	14	2.8	14	4 AAU28402	AAU28402 Peptide s
47	14	2.8	14	4 AAU25421	AAU25421 Schizophr
48	14	2.8	14	4 AAU24972	AAU24972 Schizophr
49	14	2.8	14	4 AAU26541	AAU26541 Peptide #
50	14	2.8	14	4 AAU15316	AAU15316 Schizophr
51	14	2.8	14	8 ADO78583	ADO78583 Schizophr
52	14	2.8	14	8 ADO79047	ADO79047 Schizophr
53	14	2.8	20	9 AEB45366	AEB45366 Fragment
54	14	2.2	11	4 AAU24977	AAU24977 Schizophr
55	11	2.2	11	4 AAU24971	AAU24971 Schizophr
56	11	2.2	11	4 AAU24973	AAU24973 Schizophr
57	11	2.2	11	4 AAU15321	AAU15321 Schizophr
58	11	2.2	11	4 AAU15315	AAU15315 Schizophr
59	11	2.2	11	4 AAU15317	AAU15317 Schizophr
60	11	2.2	11	8 ADO78582	ADO78582 Schizophr
61	11	2.2	11	8 ADO78584	ADO78584 Schizophr
62	11	2.2	11	8 ADO78588	ADO78588 Schizophr
63	11	2.2	415	4 ABB66250	ABB66250 Drosophil
64	11	2.2	462	4 ABB66252	ABB66252 Drosophil
65	10	2.0	10	4 AAU28403	AAU28403 Peptide s
66	10	2.0	10	4 AAU24974	AAU24974 Schizophr
67	10	2.0	10	4 AAU25422	AAU25422 Schizophr
68	10	2.0	10	4 AAU26542	AAU26542 Peptide #
69	10	2.0	10	4 AAU15318	AAU15318 Schizophr
70	10	2.0	10	8 ADO78585	ADO78585 Schizophr
71	10	2.0	10	8 ADO79049	ADO79049 Schizophr
72	10	2.0	308	8 ADO79067	ADO79067 Plant ful
73	10	2.0	318	2 AAY08759	AAY08759 L. monocy
74	10	2.0	351	7 ADM25522	ADM25522 Hyperther
75	10	2.0	379	5 ABB47976	ABB47976 Listeria
76	10	2.0	481	6 ABR52953	ABR52953 Protein s
77	10	2.0	4	7 ADK62620	ADK62620 Disease t
78	9	1.8	9	4 AAU24975	AAU24975 Schizophr
79	9	1.8	9	4 AAU15319	AAU15319 Schizophr
80	9	1.8	9	8 ADO78586	ADO78586 Schizophr
81	9	1.8	150	4 ABO03794	ABO03794 Novel hum
82	9	1.8	150	6 ABO00646	ABO00646 Novel hum
83	9	1.8	150	6 ABO00886	ABO00886 Polypepti
84	9	1.8	170	4 AAB39315	AAB39315 Human pro
85	9	1.8	194	5 AAU83607	AAU83607 Human pro
86	9	1.8	194	5 ADY31772	ADY31772 Novel hum
87	9	1.8	194	6 ABO80754	ABO80754 Human PRO
88	9	1.8	194	6 ABO33720	ABO33720 Novel hum
89	9	1.8	194	6 ABO82063	ABO82063 Novel hum
90	9	1.8	194	6 ABO72243	ABO72243 Human PRO
91	9	1.8	194	6 ABO72371	ABO72371 Human PRO
92	9	1.8	194	6 ABO34266	ABO34266 Human sec
93	9	1.8	194	7 ABO722073	ABO722073 Human mem
94	9	1.8	194	7 ADB83522	ADB83522 Novel hum
95	9	1.8	194	7 ADB80628	ADB80628 Novel hum
96	9	1.8	194	7 ADB73169	ADB73169 Novel hum
97	9	1.8	194	7 ADB78251	ADB78251 Novel hum

98	9	1.8	194	7	ADB4899	Human	PRO
99	9	1.8	194	7	ADB78005	Novel	hum
100	9	1.8	194	7	ADB87071	Human	PRO
101	9	1.8	194	7	ADB84653	Human	PRO
102	9	1.8	194	7	ADB83768	Novel	hum
103	9	1.8	194	7	ADB72923	Novel	hum
104	9	1.8	194	7	ADB36761	Human	PRO
105	9	1.8	194	7	ADB21751	Human	PRO
106	9	1.8	194	7	ADC49782	Novel	hum
107	9	1.8	194	7	ADC48981	Novel	hum
108	9	1.8	194	7	ADC49498	Novel	hum
109	9	1.8	194	7	ADC47359	Novel	hum
110	9	1.8	194	7	ADC47104	Novel	hum
111	9	1.8	194	7	ADC77979	Novel	hum
112	9	1.8	194	7	ADD06214	Novel	hum
113	9	1.8	194	7	ADC77733	Novel	hum
114	9	1.8	194	7	ADD50696	Novel	hum
115	9	1.8	194	7	ADD50942	Novel	hum
116	9	1.8	194	7	ADD50423	Novel	hum
117	9	1.8	194	7	ADD50177	Human	PRO
118	9	1.8	194	7	ADD51188	Novel	hum
119	9	1.8	194	8	ADC48735	Novel	hum
120	9	1.8	194	8	ADBE20906	Novel	hum
121	9	1.8	194	8	ADBE05750	Human	PRO
122	9	1.8	194	8	ADD74979	Human	PRO
123	9	1.8	194	8	ADD75725	Novel	hum
124	9	1.8	194	8	ADD84957	Novel	hum
125	9	1.8	194	8	ADD86783	Novel	hum
126	9	1.8	194	8	ADBE20660	Novel	hum
127	9	1.8	194	8	ADBE38957	Novel	hum
128	9	1.8	194	8	ADBE05504	Human	PRO
129	9	1.8	194	8	ADD73489	Human	PRO
130	9	1.8	194	8	ADD78329	Novel	hum
131	9	1.8	194	8	ADBE21152	Novel	hum
132	9	1.8	194	8	ADD77267	Novel	hum
133	9	1.8	194	8	ADBE20414	Novel	hum
134	9	1.8	194	8	ADD75479	Human	PRO
135	9	1.8	194	8	ADD73995	Human	PRO
136	9	1.8	194	8	ADD74241	Human	PRO
137	9	1.8	194	8	ADD75971	Novel	hum
138	9	1.8	194	8	ADBE5463	Novel	hum
139	9	1.8	194	8	ADBE05012	Human	PRO
140	9	1.8	194	8	ADD75225	Human	PRO
141	9	1.8	194	8	ADD76769	Novel	hum
142	9	1.8	194	8	ADBE6537	Novel	hum
143	9	1.8	194	8	ADD78005	Novel	hum
144	9	1.8	194	8	ADD77513	Novel	hum
145	9	1.8	194	8	ADD77759	Novel	hum
146	9	1.8	194	8	ADBE5217	Novel	hum
147	9	1.8	194	8	ADD73749	Human	PRO
148	9	1.8	194	8	ADD74487	Human	PRO
149	9	1.8	194	8	ADD77015	Novel	hum
150	9	1.8	194	8	ADBE5709	Novel	hum

ALIGNMENTS

RESULT 1
ID AAB97262 standard; protein; 508 AA.
AAB97262;

DT 08-AUG-2001 (first entry)

DE Human carnosinase.

XX Human; carnosinase; carnosine; anserine; hydrolysis; brain; epilepsy;
KW Alzheimer's disease; cognitive disorder; development abnormality;
KW foetal deficiency; neurodegenerative disorder; schizophrenia;
KW amyotrophic lateral sclerosis; Parkinson's disease; ischaemic shock.

OS Homo sapiens.
XX
XX EPI097997-A1.
XX
XX 09-MAY-2001.
XX
XX
XX 03-NOV-1999; 99EP-00402723.
XX
XX 03-NOV-1999; 99EP-00402723.
XX
XX (SNFI) SANOFI-SYNTHELABO.
XX
XX Saudak V, Smirnova-Robert T, Teufel M;
XX WPI; 2001-319238/34.
XX N-PSDB; AAF27154.
XX
XX Novel isolated human carnosinase polypeptide useful for prevention and/or
XX treatment of Alzheimer's disease, amyotrophic lateral sclerosis,
XX Parkinson's disease, schizophrenia, ischemic shock, and epilepsy.
XX
XX Claim 6, Page 19-20; 27pp; English.

CC The present sequence represents human carnosinase. Carnosinase is a
CC glycoprotein with an isoelectric point of 4.4. The active enzyme is a
CC dimer, with the two subunits being connected by at least one disulphide
CC bond. The enzyme is especially active in hydrolysing carnosine and
CC anserine. Carnosinase is found in high concentration in the brain.
CC Homocarnosine is hydrolysed in the brain, and carnosine and anserine are
CC split in the blood stream by carnosinase. Carnosine and anserine are
CC thought to act as cytosol buffering agents. Carnosinase its agonists and
CC antagonists and compositions containing them are useful for the
CC prevention and/or treatment of Alzheimer's disease and cognitive
CC disorders, development abnormalities and foetal deficiencies.
CC neurodegenerative disorders such as amyotrophic lateral sclerosis,
CC Parkinson's disease, schizophrenia, abnormal mental states, ischaemic
CC shock, and epilepsy

XX Sequence 508 AA;

Query Match 100.0%; Score 508; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 508; Conservative 0; Indels 0;

QY 1 MDPKLRMAASLAVLTLLEERGFSSPPALLEKVFQYIDHQBEPVTLKEMVAI 60
DB 1 MDPKLRMAASLAVLTLLEERGFSSPPALLEKVFQYIDHQBEPVTLKEMVAI 60
QY 61 ESDSVQVPRFRQELFRMVAADTLQRLGARVASVDMGPQQLPPGGSUPLPPVLAELG 120
DB 61 ESDSVQVPRFRQELFRMVAADTLQRLGARVASVDMGPQQLPPGGSUPLPPVLAELG 120
QY 121 SPTGTGTCFPGHLDVOPADRGDGLTPPYVLTEDGKLYGAGADNKGPAVLAMINAVSA 180
DB 121 SPTGTGTCFPGHLDVOPADRGDGLTPPYVLTEDGKLYGAGADNKGPAVLAMINAVSA 180
QY 181 FRALRQDLPVNIKFIIEGMEAGSVALLEVEKEKDRFFSGVDYIVISDNLMISQKPAI 240
DB 181 FRALRQDLPVNIKFIIEGMEAGSVALLEVEKEKDRFFSGVDYIVISDNLMISQKPAI 240
QY 241 TYGTRGNSYFWEVCKCRQDPSGTFGGIILHEPMADVLALLGSLVDSGHLVPGIYBEV 300
DB 241 TYGTRGNSYFWEVCKCRQDPSGTFGGIILHEPMADVLALLGSLVDSGHLVPGIYBEV 300
QY 301 VPLTEELINTYKAHLDEEYRNSGRVEKFLPDTKEEILMLMRPVSIIHGIEGAFDEP 360
DB 301 VPLTEELINTYKAHLDEEYRNSGRVEKFLPDTKEEILMLMRPVSIIHGIEGAFDEP 360
QY 361 GKTIVIPGRVIGKFSIRLVPMNVSAVEKQYTRHLEDVFSKRNSSNNKVVSTGLGHPMI 420
DB 361 GKTIVIPGRVIGKFSIRLVPMNVSAVEKQYTRHLEDVFSKRNSSNNKVVSTGLGHPMI 420
QY 421 ANIDTQYLAARAIITVGTGEPDMIRDSITIPAKMQELVHKSVLPLGADVDEGHS 480

Db 421 ANIDDTQYLAARAIKRTVFGTEPDMIRDSSTPIAKMFOEIVHKSVALPLGAVDDGSHS 480
 QY 481 ONEKINRMNYIEGSKLPAAFFLEMAQLH 508
 Db 481 ONEKINRMNYIEGSKLPAAFFLEMAQLH 508

RESULT 2

AAG89122
 ID AAG89122 standard; protein; 508 AA.

AC AAG89122;

XX 11-SEP-2001 (first entry)

XX Human secreted protein, SEQ ID NO: 242.

XX Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;

XX GENSET.

XX Homo sapiens.

XX MO200142451-A2.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000MO-IB001938.

XX 08-DEC-1999; 99US-0169629P.

XX 06-MAR-2000; 2000US-0187470P.

XX (GEST) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S;

DR WPI; 2001-367870/38.

DR N-PSDB; AAH64725.

PT Full length GENSET human nucleic acids encoding potentially secreted

PT proteins, useful in gene therapy and vaccination against a variety of

PT diseases, and for diagnosis of those diseases.

XX Claim 21; Page 791-792; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding

XX potentially secreted proteins. The nucleic acids and the polypeptides

XX they encode may be used in the prevention, treatment and diagnosis of

XX diseases associated with inappropriate GENSET gene expression. For

XX example, they be used to treat disorders associated with decreased GENSET

XX gene expression by rectifying mutations or deletions in a patient's

XX genome that affect the activity of GENSET or by supplementing the

XX patient's own production of GENSET polypeptides. Conversely, antisense

XX nucleic acid molecules may be administered to down regulate GENSET

XX expression by binding with the cells' own genes and preventing their

XX expression. The sense and antisense nucleic acids may also be used as DNA

XX probes in diagnostic assays to detect and quantitate the presence of

XX similar nucleic acid sequences in samples, and hence to determine which

XX patients may be in need of restorative therapy. The GENSET polypeptides

XX may be used as antigens in the production of antibodies and in assays to

XX identify modulators (agonists and antagonists) of GENSET polypeptide

XX expression and activity. The present sequence is a GENSET polypeptide of

XX the invention

XX Sequence 508 AA.

SO Query Match 100.0%; Score 508; DB 4; Length 508;

SO Best Local Similarity 100.0%; Pred. No. 0;

SO Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRKLGMAASLLAVLLILLERGMSSPPPALLEKFOYIDLHODEFVQTLKEMVAI 60

Db 1 MDRKLGMAASLLAVLLILLERGMSSPPPALLEKFOYIDLHODEFVQTLKEMVAI 60

QY 61 ESDSVQVPRFRQELFRMMAVAADTLQRLGARVASYDMGQQLPDGQSLPIPPVILAEIG 120

Db 61 ESDSVQVPRFRQELFRMMAVAADTLQRLGARVASYDMGQQLPDGQSLPIPPVILAEIG 120

QY 121 SDPTKGTVCYGHLDVQPADRGDWLTDPVYLTEVQKLYGRGATDNKGAVLAMINAVSA 180

Db 121 SDPTKGTVCYGHLDVQPADRGDWLTDPVYLTEVQKLYGRGATDNKGAVLAMINAVSA 180

QY 181 FRALBODLPVNIKFIIEGMEAGSVALBEIVKEXKORFSGVDYIYISDNLMTISQKPAI 240

Db 181 FRALBODLPVNIKFIIEGMEAGSVALBEIVKEXKORFSGVDYIYISDNLMTISQKPAI 240

QY 241 TYGTRGNSYFMVAVKRDODFHSGTGGLIHEPMALVALLGSLDSSGHIIVPGIYDEV 300

Db 241 TYGTRGNSYFMVAVKRDODFHSGTGGLIHEPMALVALLGSLDSSGHIIVPGIYDEV 300

QY 301 VPLTESEINTYKAIHDLSEYRNSRVEKFLPTKEIIMHLMRYPSLSIHGIEGAFDEP 360

Db 301 VPLTESEINTYKAIHDLSEYRNSRVEKFLPTKEIIMHLMRYPSLSIHGIEGAFDEP 360

QY 361 GTKTVIPGRVIGKFSIRLYPHMNVSAVEKQVTRHLEDVFSKNSNKMVVSMTLGLHPWI 420

Db 361 GTKTVIPGRVIGKFSIRLYPHMNVSAVEKQVTRHLEDVFSKNSNKMVVSMTLGLHPWI 420

QY 421 ANIDDTQYLAARAIKRTVFGTEPDMIRDSSTPIAKMFOEIVHKSVALPLGAVDDGSHS 480

Db 421 ANIDDTQYLAARAIKRTVFGTEPDMIRDSSTPIAKMFOEIVHKSVALPLGAVDDGSHS 480

QY 481 ONEKINRMNYIEGSKLPAAFFLEMAQLH 508

Db 481 ONEKINRMNYIEGSKLPAAFFLEMAQLH 508

RESULT 3

ABR47759

ID ABR47759 standard; protein; 508 AA.

XX ABR47759;

AC ABR47759;

XX 12-JUN-2003 (first entry)

XX Human secreted protein, SEQ ID 650.

XX Human secreted protein, SEQ ID 650.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;

XX KX vulnerable; antiinflammatory; nootropic; neuroprotective;

XX antiParkinsonian; gene therapy; human; cardiovascular disorder.

XX Homo sapiens.

XX MO200295010-A2.

XX 28-NOV-2002.

XX 19-MAR-2002; 2002MO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,

XX PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular

XX disorders such as arrhythmia.

XX Claim 13; SEQ ID NO 650; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47753-

CC ABR4145) and their coding sequences (ACC50344-ACC50856). The proteins
CC or their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders, immune
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 508 AA:

Query Match 100.0%; Score 508; DB 6; Length 508;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLAVLTLLELRGMFSSPPPALLEKVFQYIDLDHODEFVQTLKEWVAI 60
DB 1 MDPKLGMAASLAVLTLLELRGMFSSPPPALLEKVFQYIDLDHODEFVQTLKEWVAI 60
QY 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQOLPDGOSLPPIPVILAEIG 120
DB 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQOLPDGOSLPPIPVILAEIG 120
QY 121 SDPTKGTVCFGHLDVQPADRGDGLTDPPVLTTEVDGKLYRGATDNKGPTLAWINAVSA 180
DB 121 SDPTKGTVCFGHLDVQPADRGDGLTDPPVLTTEVDGKLYRGATDNKGPTLAWINAVSA 180
QY 181 PRALBEDLPVNIKEITIEGMEBAGVALLELVEKEKRFSGVDYIYISNLMISQKKPAI 240
DB 181 PRALBEDLPVNIKEITIEGMEBAGVALLELVEKEKRFSGVDYIYISNLMISQKKPAI 240
QY 241 TYGTRGNSYFMVEVKCRDDFHSGTFGILHEPMADLVALLGSLVDSGHIIPGIIYDEV 300
DB 241 TYGTRGNSYFMVEVKCRDDFHSGTFGILHEPMADLVALLGSLVDSGHIIPGIIYDEV 300
QY 301 VPLTEBEINTYKAIHLDLEBYRNSVVEKFLPTKEEILMHLWRYPSLSIHGIEGAFDEP 360
DB 301 VPLTEBEINTYKAIHLDLEBYRNSVVEKFLPTKEEILMHLWRYPSLSIHGIEGAFDEP 360
QY 361 GRTKTVIPGRVIGKFSIRLVPNMVSAVEKQVTRHLEDVFSKRNSSKMMVSMTLGIHPMI 420
DB 361 GRTKTVIPGRVIGKFSIRLVPNMVSAVEKQVTRHLEDVFSKRNSSKMMVSMTLGIHPMI 420
QY 421 ANIDDTQYLAARKAIRTVGTGEBDMIRDSTIPIAKFOEIVHKSIVLLPLGAVDGEHS 480
DB 421 ANIDDTQYLAARKAIRTVGTGEBDMIRDSTIPIAKFOEIVHKSIVLLPLGAVDGEHS 480
QY 481 ONEKINRWNYIESTKLPAAFFLEMAQLH 508
DB 481 ONEKINRWNYIESTKLPAAFFLEMAQLH 508

RESULT 4

ABR00082 standard; protein; 508 AA.

AC ABR00082;

XX 03-APR-2003 (first entry)

XX Human gene 72 encoded secreted protein HRPEN62, SEQ ID NO:371.
XX Human; secreted protein; digestive disorder; gastrointestinal disorder;
XX mouth; oesophagus; stomach; small intestine; large intestine; liver;
XX biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
XX immune disorder; inflammation; infection; wound healing; drug screening;
XX chromosome identification; chromosome mapping; cytostatic;
XX antiinflammatory; immunosuppressive; vulnery; gene therapy.
OS Homo sapiens.
XX WO200276486-A1.
XX 03-OCT-2002.
XX 19-MAR-2002; 2002MO-US008276.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2003-029900/02.
XX N-PSDB; ABZ71261.
XX New human secreted proteins and nucleic acids, useful for detecting,
XX preventing, diagnosing, prognosticating, treating and/or ameliorating
XX e.g. gastrointestinal diseases and disorders, or cancers.
XX Claim 13; Page 984-986; 1216pp; English.

ABZ71130-ABZ71478 represent cDNAs corresponding to 178 human secreted
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening, and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing, treating, ameliorating or preventing
CC digestive disorders. Such conditions include disorders of the mouth,
CC oesophagus, stomach, small intestine, large intestine, liver, biliary
CC tract and pancreas, and include cancers of these organs and tissues. The
CC secreted proteins and their nucleic acids may also be used in the
CC treatment of immune disorders, inflammation, infection,
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
CC of the invention may be used for chromosome identification, chromosome
CC mapping, in gene therapy, for identifying individuals from minute
CC biological samples, as hybridisation probes, and as molecular weight
CC markers. The present sequence represents a human secreted protein of the
CC invention

XX Sequence 508 AA:

Query Match 100.0%; Score 508; DB 6; Length 508;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLAVLTLLELRGMFSSPPPALLEKVFQYIDLDHODEFVQTLKEWVAI 60
DB 1 MDPKLGMAASLAVLTLLELRGMFSSPPPALLEKVFQYIDLDHODEFVQTLKEWVAI 60
QY 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQOLPDGOSLPPIPVILAEIG 120
DB 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQOLPDGOSLPPIPVILAEIG 120
QY 121 SDPTKGTVCFGHLDVQPADRGDGLTDPPVLTTEVDGKLYRGATDNKGPTLAWINAVSA 180
DB 121 SDPTKGTVCFGHLDVQPADRGDGLTDPPVLTTEVDGKLYRGATDNKGPTLAWINAVSA 180

QY 181 FRALBQDLPVNLIKFIIEGMEBAGSVALBELVEKEDRPFSGVDYIVISDNLMISQKRPAT 240
 DB 181 FRALBQDLPVNLIKFIIEGMEBAGSVALBELVEKEDRPFSGVDYIVISDNLMISQKRPAT 240
 QY 241 TYGTRGNSYFMWVEVKCRDODFHSCTFGGILHEPMADVLALLGSLVDSGHIIVPGIYDEV 300
 DB 241 TYGTRGNSYFMWVEVKCRDODFHSCTFGGILHEPMADVLALLGSLVDSGHIIVPGIYDEV 300
 QY 301 VPLTEESINTYKAHLDLEERYNRSRYEKPLFTQKEIILMHLMRYPSLSIHGIEGADDP 360
 DB 301 VPLTEESINTYKAHLDLEERYNRSRYEKPLFTQKEIILMHLMRYPSLSIHGIEGADDP 360
 QY 361 GRTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKNNSNMVSMTLGLHPWI 420
 DB 361 GRTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKNNSNMVSMTLGLHPWI 420
 QY 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTPIAKMFOEIVHKSIVLLIPGAVDDGHS 480
 DB 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTPIAKMFOEIVHKSIVLLIPGAVDDGHS 480
 QY 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508
 DB 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508

RESULT 5

ADB91551
 ID ADB91551 standard; protein; 508 AA.

AC ADB91551;

DT 04-DEC-2003 (first entry)

DE Human secreted protein #SEQ ID 497.

KX Secreted protein; gene therapy; antidiabetic; diabetes; human.

OS Homo sapiens.

PN W02003004622-A2.

PD 16-JAN-2003.

PF 19-MAR-2002; 2002WC-US008124.

PR 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM,

DR WPI; 2003-229407/22.

PT Nucleic acid encoding a human secreted protein is useful in diagnosing or

PT treating diabetes or conditions related to diabetes.

PS Claim 3; SEQ ID NO 497; 1537bp; English.

XX The invention relates to isolated nucleic acid molecules ADB91065-

CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-

CC ADB91834. Also disclosed is a recombinant vector comprising a

CC polynucleotide of the invention, and a recombinant host cell comprising

CC the recombinant vector. The polypeptide of the invention is useful in

CC identifying a binding partner by contacting the polypeptide with a

CC binding partner, and determining whether the binding partner increases or

CC decreases activity of the polypeptide. The polypeptide, polynucleotide,

CC antibody or its fragment, agonist or antagonist are useful for preparing

CC a pharmaceutical composition for diagnosing or treating diabetes or

CC conditions related to diabetes. The present sequence is that of the human

CC immunoglobulin Fc portion used to generate fusion proteins, increasing

CC the stability of the fused protein as compared to the secreted protein

CC only. Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPD at fcp.wipo.int/pub/published_pcc_sequences.

CC XX Sequence 508 AA;

QY Query Match 100.0%; Score 508; DB 7; Length 508;

DB Best Local Similarity 100.0%; Pred No. 0;

Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKGRMASLILAVLLILLERGMFSSPPALIEKYQYIDLHQDEFVOTLKEMVAI 60

DB 1 MDPKGRMASLILAVLLILLERGMFSSPPALIEKYQYIDLHQDEFVOTLKEMVAI 60

QY 61 ESDSVQPVPRFROELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIG 120

DB 61 ESDSVQPVPRFROELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIG 120

QY 121 SDPTKGTVCFGHLDVQPADRGDWLTDPYVLTENVGKLYGSGATDNKGPVLAITNAVSA 180

DB 121 SDPTKGTVCFGHLDVQPADRGDWLTDPYVLTENVGKLYGSGATDNKGPVLAITNAVSA 180

QY 181 FRALBQDLPVNLIKFIIEGMEBAGSVALBELVEKEDRPFSGVDYIVISDNLMISQKRPAT 240

DB 181 FRALBQDLPVNLIKFIIEGMEBAGSVALBELVEKEDRPFSGVDYIVISDNLMISQKRPAT 240

QY 241 TYGTRGNSYFMWVEVKCRDODFHSCTFGGILHEPMADVLALLGSLVDSGHIIVPGIYDEV 300

DB 241 TYGTRGNSYFMWVEVKCRDODFHSCTFGGILHEPMADVLALLGSLVDSGHIIVPGIYDEV 300

QY 301 VPLTEESINTYKAHLDLEERYNRSRYEKPLFTQKEIILMHLMRYPSLSIHGIEGADDP 360

DB 301 VPLTEESINTYKAHLDLEERYNRSRYEKPLFTQKEIILMHLMRYPSLSIHGIEGADDP 360

QY 361 GRTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKNNSNMVSMTLGLHPWI 420

DB 361 GRTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKNNSNMVSMTLGLHPWI 420

QY 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTPIAKMFOEIVHKSIVLLIPGAVDDGHS 480

DB 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTPIAKMFOEIVHKSIVLLIPGAVDDGHS 480

QY 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508

DB 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508

RESULT 6

ADCT4152

ID ADCT4152 standard; protein; 508 AA.

AC ADCT4152;

DT 01-JAN-2004 (first entry)

DE Human secreted protein - SEQ ID 785.

KX antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;

KX antidiabetic; immunosuppressive; dermatological; nephrotoxic;

KX antiparkinsonian; neuroprotective; neurotoxic; antibacterial; virucide;

KX fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;

KX haemopoietic; haematologic; anaemia; autoimmune disorder;

KX rheumatoid arthritis; inflammation; Grave's disease; diabetes;

KX systemic lupus erythematosus; glomerulonephritis; neurodegenerative;

KX Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;

KX cancer; bacterial; viral; fungal; parasitic infection; gene therapy;

OS human.

OS Homo sapiens.

XX W02003038063-A2.

PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 PS Claim 11; SEQ ID NO 139; 453bp; English.
 CC The invention relates to human secreted polypeptides and the
 CC polynucleotides encoding them. The sequences are useful for preparing
 CC medicaments for preventing, treating or ameliorating medical conditions
 CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
 CC as Alzheimer's disease. This sequence represents a human secreted
 CC polypeptide of the invention.
 XX
 SQ Sequence 508 AA;
 Query Match 100.0%; Score 508; DB 7; Length 508;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
 DB 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
 QY 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
 DB 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
 QY 121 SDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGKATDNKGPVLAMINAVSA 180
 DB 121 SDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGKATDNKGPVLAMINAVSA 180
 QY 181 FRALEQDLPVNIKFIIEGMEBAGSVALBELVEKEKDRFFSGVDYIVISDNLMISQKPAI 240
 DB 181 FRALEQDLPVNIKFIIEGMEBAGSVALBELVEKEKDRFFSGVDYIVISDNLMISQKPAI 240
 QY 241 TYGKRGNSYFVPRVYKCDOPHSGTSGGILHEPMADVLALIGSLVDSGGHILVPGIYDEV 300
 DB 241 TYGKRGNSYFVPRVYKCDOPHSGTSGGILHEPMADVLALIGSLVDSGGHILVPGIYDEV 300
 QY 301 VPLTEEBINTYKAHLHLEERYNSRYEKFPLDTKEELIMLWYPSLSIHGIEGAFDEP 360
 DB 301 VPLTEEBINTYKAHLHLEERYNSRYEKFPLDTKEELIMLWYPSLSIHGIEGAFDEP 360
 QY 361 GTKTVIPGRVIGKFSIRLVPMNVSAVEKQVTRLEDFVFSRNSNNQVSMTLGLHPWI 420
 DB 361 GTKTVIPGRVIGKFSIRLVPMNVSAVEKQVTRLEDFVFSRNSNNQVSMTLGLHPWI 420
 QY 421 ANIDDTQYLAAKAIRVFGTEPMDIGSTIPIAKKFOEIVHKSIVLIPGAVDGEHS 480
 DB 421 ANIDDTQYLAAKAIRVFGTEPMDIGSTIPIAKKFOEIVHKSIVLIPGAVDGEHS 480
 QY 481 QNEKINRWNYIEGTLFAAFPLEMAQLH 508
 DB 481 QNEKINRWNYIEGTLFAAFPLEMAQLH 508
 RESULT 8
 ID AAY76144 standard; protein: 509 AA.
 XX AAY76144;
 AC AAY76144;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human secreted protein encoded by gene 21.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmunity; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; chromosome 18q22-23.
 XX

OS Homo sapiens.
 XX
 PN WO958660-A1.
 XX
 XX 18-NOV-1999.
 PD
 XX
 PF 06-MAY-1999; 99MO-US009847.
 XX
 PR 12-MAY-1998; 98US-0085093P.
 PR 12-MAY-1998; 98US-0085094P.
 PR 12-MAY-1998; 98US-0085105P.
 PR 12-MAY-1998; 98US-0085180P.
 PR 18-MAY-1998; 98US-0085906P.
 PR 18-MAY-1998; 98US-0085920P.
 PR 18-MAY-1998; 98US-0085921P.
 PR 18-MAY-1998; 98US-0085922P.
 PR 18-MAY-1998; 98US-0085923P.
 PR 18-MAY-1998; 98US-0085924P.
 PR 18-MAY-1998; 98US-0085925P.
 PR 18-MAY-1998; 98US-0085927P.
 PR 18-MAY-1998; 98US-0085928P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
 PI Endreess GA, Ebner R;
 XX
 DR WPI; 2000-062236/05.
 DR N-PSDB; AAZ65270.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 PS
 XX Claim 11; Page 373-374; 475bp; English.
 XX
 CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human
 CC genes. The gene encoding this protein was found to be on chromosome 18q22
 CC -23. The genes and their corresponding secreted polypeptides are useful
 CC for preventing, treating or ameliorating medical conditions, e.g. by
 CC protein or gene therapy. Also pathological conditions can be diagnosed by
 CC determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 97 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
 CC
 XX
 SQ Sequence 509 AA;
 Query Match 100.0%; Score 508; DB 3; Length 509;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
 DB 1 MDPKLGMAASLLAVLLLLLLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
 QY 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
 DB 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
 QY 121 SDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGKATDNKGPVLAMINAVSA 180
 DB 121 SDPTKGTVCFYGHLDVQPADRGDGLTDPYVLTVEVDGKLYGKATDNKGPVLAMINAVSA 180

QY 181 FRALEDLPVNIKFIIEGEEAGSVALEBELVEKORFPGSGVDYIVISDNLMISORKPAI 240
 CC (which modulates protease activity in vitro) may be used to treat a
 CC disease or disorder selected from cancers (e.g., of tissues, of blood or
 CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
 CC brain, ovarian, bladder or kidney), immune-related diseases and
 CC disorders, cardiovascular disease, brain or neuronal diseases associated
 CC (e.g., central or peripheral nervous system diseases, migraine, pain,
 CC sexual dysfunction, mood disorders, attention disorders, cognition
 CC disorders, hypotension, hypertension, psychotic disorders, neurological
 CC disorders and dyskinesias), metabolic disorders and inflammatory
 CC disorders. (I) may also be useful as a diagnostic tool for a disease or
 CC disorder, such as those above. AAU72910 represent human protease
 CC amino acid sequences of the invention
 CC XX

QY 241 TVGTGRNSYMWVWKCRDQFHSCTGGIIEHPMADLVALLGSLVNSSGHILVPGIYDEV 300
 Db 241 TVGTGRNSYFMVWVKCRDQFHSCTGGIIEHPMADLVALLGSLVNSSGHILVPGIYDEV 300
 QY 301 VPLTESEINTYKAIHLDLEERNSRVEKFLPTKEEILMHLWRYPSSLHGIEGAFDEP 360
 Db 301 VPLTESEINTYKAIHLDLEERNSRVEKFLPTKEEILMHLWRYPSSLHGIEGAFDEP 360
 QY 361 GIKTVIPGRVIGKFSIRLVPMNVSAVEKQVTRHLEDFVSKRNSNMVVSMTGLHPMI 420
 Db 361 GIKTVIPGRVIGKFSIRLVPMNVSAVEKQVTRHLEDFVSKRNSNMVVSMTGLHPMI 420
 QY 421 ANIDDPQYLAARAIITVGTCTEPDMIRDGSTPIAKMFGQIVHKSIVLIPGAVDGEHS 480
 Db 421 ANIDDPQYLAARAIITVGTCTEPDMIRDGSTPIAKMFGQIVHKSIVLIPGAVDGEHS 480
 QY 481 ONEKINRMNIEGSKLFAAFLEMAQLH 508
 Db 481 ONEKINRMNIEGSKLFAAFLEMAQLH 508

RESULT 9
 AAU72908
 ID AAU72908 standard; protein; 507 AA.
 XX AAU72908;
 AC

DT 26-FEB-2002 (first entry)
 XX
 DE Human metalloprotease partial protein sequence #20.
 XX

KM Human; protease; PCR primer; cytosolic; immunomodulator; cardiant;
 KM vasoactive; antihypertensive; analgesic; endocrine; nootropic; tranquiliser;
 KM hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
 KM anorectic; antiinflammatory; aspartyl protease; cysteine protease;
 KM metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
 KM lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
 KM immune-related disease; cardiovascular disease; neuronal disease;
 KM migraine; sexual dysfunction; mood disorder; attention disorder;
 KM cognition disorder; hypotension; hypertension; psychotic disorder;
 KM dyskinesia; metabolic disorder; inflammatory disorder.

OS Homo sapiens.
 XX
 PN WO200183782-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 04-MAY-2001; 2001MO-US014431.
 XX
 PR 04-MAY-2000; 2000US-0201879P.
 XX

XX (SUGEN-) SUGEN INC.
 PA Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S,
 PI Payne V,
 DR WPI; 2002-041502/05.
 XX N-PSDB; AAS97191.
 XX

PT Novel protease polypeptide useful for screening for substances that may
 PT be used to treat, e.g., cancers, immune-related diseases, cardiovascular
 PT disease, migraine, pain, psychotic and inflammatory disorders.
 XX

PS Claim 28; Fig 21; 232pp; English.

CC The invention relates to an isolated, enriched, or purified protease
 CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to

CC screen for substances (S) that may modulate its activity. Administering S
 CC (which modulates protease activity in vitro) may be used to treat a
 CC disease or disorder selected from cancers (e.g., of tissues, of blood or
 CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
 CC brain, ovarian, bladder or kidney), immune-related diseases and
 CC disorders, cardiovascular disease, brain or neuronal diseases associated
 CC (e.g., central or peripheral nervous system diseases, migraine, pain,
 CC sexual dysfunction, mood disorders, attention disorders, cognition
 CC disorders, hypotension, hypertension, psychotic disorders, neurological
 CC disorders and dyskinesias), metabolic disorders and inflammatory
 CC disorders. (I) may also be useful as a diagnostic tool for a disease or
 CC disorder, such as those above. AAU72876-AAU72910 represent human protease
 CC amino acid sequences of the invention
 CC XX

Sequence 507 AA;

Query Match 96.9%; Score 492; DB 5; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLEKGMFSSPPSPALLEKVFQYIDHODEFVQTLKEWVAIESDVQVPRPROELF 76
 Db 16 LLLLEKGMFSSPPSPALLEKVFQYIDHODEFVQTLKEWVAIESDVQVPRPROELF 75
 QY 77 RMAVAADTLQRLGARVASVDMGPQQLPDGSLPIPVITLAEISDPKGTVCYGHLDV 136
 Db 76 RMAVAADTLQRLGARVASVDMGPQQLPDGSLPIPVITLAEISDPKGTVCYGHLDV 135
 QY 137 QPADRGDGLTDPVYLVTEVDGKLVYRGATDNKGPULAMINVASARALEODLPVNIKFI 196
 Db 136 QPADRGDGLTDPVYLVTEVDGKLVYRGATDNKGPULAMINVASARALEODLPVNIKFI 195
 QY 197 EGMEEAGSVALEBELVEKEDRFFSGVDYIVISDNLMISORKPAITYGTGRNSYFMVWVKC 256
 Db 196 EGMEEAGSVALEBELVEKEDRFFSGVDYIVISDNLMISORKPAITYGTGRNSYFMVWVKC 255
 QY 257 RDQDHSCTGGIIEHPMADLVALLGSLVNSSGHILVPGIYDEVVPLTBESEINTYKAIHL 316
 Db 256 RDQDHSCTGGIIEHPMADLVALLGSLVNSSGHILVPGIYDEVVPLTBESEINTYKAIHL 315
 QY 317 DLEERNSRVEKFLPTKEEILMHLWRYPSSLHGIEGAFDEPQTVIGRVIGKFSI 376
 Db 316 DLEERNSRVEKFLPTKEEILMHLWRYPSSLHGIEGAFDEPQTVIGRVIGKFSI 375
 QY 377 RLVPMNVSAVEKQVTRHLEDFVSKRNSNMVVSMTGLHPMIANIDDTQYLAARAIR 436
 Db 376 RLVPMNVSAVEKQVTRHLEDFVSKRNSNMVVSMTGLHPMIANIDDTQYLAARAIR 435
 QY 437 TVGTCTEPDMIRDGSTPIAKMFGQIVHKSIVLIPGAVDGEHSONEKINRMNIEGSKL 496
 Db 436 TVGTCTEPDMIRDGSTPIAKMFGQIVHKSIVLIPGAVDGEHSONEKINRMNIEGSKL 495
 QY 497 FAAFLEMAQLH 508
 Db 496 FAAFLEMAQLH 507

RESULT 10
 ABB07950
 ID ABB07950 standard; protein; 507 AA.
 XX ABB07950;
 AC
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Human metalloprotease, 55054.
 XX
 KW 55054; human; metalloprotease; neural cell; cerebral injury; vulnerability;
 KM enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200226948-A2.

XX 04-APR-2002.
 PD 25-SEP-2001, 2001WO-US030016.
 XX 25-SEP-2000, 2000US-0235055P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Kapeller-Libermann R;
 PI WPI, 2002-405051/43.
 XX N-PSDB; ABL58476, ABL58477.
 DR
 XX
 PT Identifying modulator of neural cell growth or transition metal
 PT neurotoxicity, involves contacting test compound with novel human
 PT metalloprotease polypeptide and determining if the polypeptide binds the
 PT test compound.
 PS Claim 21, Fig 1A-D; 105pp; English.
 XX
 CC The invention provides a method for identifying a modulator of neural
 CC cell growth, cerebral injury or wound healing, transition metal
 CC neurotoxicity, histamine production, neural/hepatic cell proliferation or
 CC degradation of extracellular matrix, neurotransmitter or soluble
 CC intracellular/extracellular dipeptide. The method involves contacting a
 CC test compound and metalloprotease polypeptide, selected from a human
 CC metalloprotease polypeptide, termed 55054, and determining if 55054 binds
 CC the test compound. The metalloprotease, 55054 is useful for making a
 CC pharmaceutical composition for inhibiting the ability of a cell selected
 CC from a neural cell such as glial cell or neuron (a sensory neuron or
 CC olfactory sensory neuron), astrocyte, oligodendrocyte and ensheathing
 CC cell, to cleave a polypeptide. The present sequence represents the human
 CC metalloprotease, 55054
 CC
 XX
 SQ Sequence 507 AA.

Query Match 96.9%; Score 492; DB 5; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLERGMFSSPPSPALLLEKVFQYIDLHQDEFVQTLKEMVAIESDVQVPRFRQELP 76
 DB 16 LLLLLERGMFSSPPSPALLLEKVFQYIDLHQDEFVQTLKEMVAIESDVQVPRFRQELP 75
 QY 77 RMAVAADTLQRLGARVASYDMGPQQLPDQSLPIPIVILAEIGSDPTKGTVCFYGHLDV 135
 DB 76 RMAVAADTLQRLGARVASYDMGPQQLPDQSLPIPIVILAEIGSDPTKGTVCFYGHLDV 135
 QY 137 QPADRGDMLTDPYVLTENVGKLYGRGATNKGVPVLAIVASAPRLBODLPVNIKEFI 196
 DB 136 QPADRGDMLTDPYVLTENVGKLYGRGATNKGVPVLAIVASAPRLBODLPVNIKEFI 195
 QY 197 EGMEEAGSVALBELVEKEKORFFSGVDYIYISDNLMWISQKPAITTYGTRNSYFMVEVKC 256
 DB 196 EGMEEAGSVALBELVEKEKORFFSGVDYIYISDNLMWISQKPAITTYGTRNSYFMVEVKC 255
 QY 257 RDDDFHSCTGGTILHEMADLVALLGSLVDSSGHIILVPGIYDEVVPLTEEEINTYTAIHL 316
 DB 256 RDDDFHSCTGGTILHEMADLVALLGSLVDSSGHIILVPGIYDEVVPLTEEEINTYTAIHL 315
 QY 317 DLBEYRNSRVEKFLFDYTKKEIIMHLWRYPSTLHIGIEGAFDEPGTKTVI RGRVIGKFSI 376
 DB 316 DLBEYRNSRVEKFLFDYTKKEIIMHLWRYPSTLHIGIEGAFDEPGTKTVI RGRVIGKFSI 375
 QY 377 RLVPKHNVSASVEKQVTRHLEDVFSKRNSSNKVWVSMTLGLHPVIANIDTQYLAARAIR 436
 DB 376 RLVPKHNVSASVEKQVTRHLEDVFSKRNSSNKVWVSMTLGLHPVIANIDTQYLAARAIR 435
 QY 437 TVEGTSPDMTRDGGSTPIPIAKMFOEIVHKSVVILPLGAVDDGESSONEKINRWYIGSTKL 496
 DB 436 TVEGTSPDMTRDGGSTPIPIAKMFOEIVHKSVVILPLGAVDDGESSONEKINRWYIGSTKL 495

QY 497 FAFPLEMAQLH 508
 DB 496 FAFPLEMAQLH 507

RESULT 11
 ABU69115
 ID ABU69115 standard; protein, 507 AA.
 XX
 AC ABU69115;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #13.
 XX
 KW Human, secreted and transmembrane protein, bone disorder; obesity;
 KW cartilage disorder; sports injury; arthritis; diabetes mellitus;
 KW hypo-insulinaemia; obesity; hyper-insulinaemia; chylasaemia;
 KW haemoglobin-associated disorder; kidney disorder; Berger disease;
 KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
 KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;
 KW antichratic; antidiabetic; antianaemic; nephrotoxic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN US2003032061-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 26-DEC-2001, 2001US-00036214.
 XX
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 22-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 23-DEC-1998; 98US-0114140P.
 PR 12-JAN-1999; 98US-0115522P.
 PR 22-JAN-1999; 98US-0116843P.
 PR 23-MAR-1999; 98US-0125774P.
 PR 23-MAR-1999; 98US-0125778P.
 PR 24-MAR-1999; 98US-0125826P.
 PR 31-MAR-1999; 98US-0127035P.
 PR 05-APR-1999; 98US-0127066P.
 PR 13-APR-1999; 98US-0129122P.
 PR 21-APR-1999; 98US-0130359P.
 PR 27-APR-1999; 98US-0131270P.
 PR 27-APR-1999; 98US-0131272P.
 PR 27-APR-1999; 98US-0131291P.
 PR 04-MAY-1999; 98US-0132371P.
 PR 04-MAY-1999; 98US-0132379P.
 PR 14-MAY-1999; 98US-0132383P.
 PR 25-MAY-1999; 98US-0135703P.
 PR 08-JUN-1999; 98US-0138166P.
 PR 20-JUL-1999; 98US-0144791P.
 PR 03-AUG-1999; 98US-0146970P.
 PR 29-OCT-1999; 98US-0162506P.
 PR 02-DEC-1999; 98US-01628551.
 PR 22-DEC-1999; 98US-01628551.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 22-MAR-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023522.
 PR 01-DEC-2000; 2000WO-US033678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.

PR 09-UTL-2001, 2001MO-US021735.
PR 16-AUG-2001, 2001US-00931836.
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341962/32.
DR N-PSDB; ACA06168.
XX
XX
PT Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
PT PRO1887, PRO1785, PRO4353, useful for treating sports injuries,
PT arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
XX
XX Claim 12; Fig 26; 194pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or treating
CC various bone and/or cartilage disorders (e.g. sports injuries,
CC arthritis), various insulin deficient states (e.g. diabetes mellitus,
CC hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
CC disorders (e.g. thalassemias), kidney disorders, associated with
CC decreased mesangial cell function (e.g. Berger disease), or other
CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
CC sequences may be used as hybridisation probes in chromosome and gene
CC mapping, or in generating antisense RNA and DNA. They are also useful in
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, to generate transgenic animals or
CC knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification, and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO polypeptides, or for the affinity
CC purification of the polypeptides from recombinant cell culture or natural
CC sources. ABU69103-ABU69125 represent the human PRO polypeptides of the
CC invention
XX
XX Sequence 507 AA;
SQ
Query Match 96.9%; Score 492; DB 6; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 LLLLLERGMFSSPPALLERKFOYIIDLHODEFVOTLKEMVAIESDSVQPPRRQELF 76
DB 16 LLLLEERGMFSSPPALLERKFOYIIDLHODEFVOTLKEMVAIESDSVQPPRRQELF 75
QY 77 RMAVAADLTQRLGAVASVDKMPQQLPFGQSLPIPVLLAEIGSPPTGTCFCFGLHLY 136
DB 76 RMAVAADLTQRLGAVASVDKMPQQLPFGQSLPIPVLLAEIGSPPTGTCFCFGLHLY 135
QY 137 QPADRGDGLWLTDPYVLTVDGKLKYGKATDNKGPVLAMINAVAFALBODLPVNLIKFI 196
DB 136 QPADRGDGLWLTDPYVLTVDGKLKYGKATDNKGPVLAMINAVAFALBODLPVNLIKFI 195
QY 197 EGMEEKGSVALLELVKEDRPFSSGVYIVISNMLISQKRALITGTGNSYFMWEVKC 256
DB 196 EGMEEKGSVALLELVKEDRPFSSGVYIVISNMLISQKRALITGTGNSYFMWEVKC 255
QY 257 RQDDFHSSTFGGILHPMADLVALLGSLVDSGHIIVPGIYDEVVPLTEEBINTYKAIHL 316
DB 256 RQDDFHSSTFGGILHPMADLVALLGSLVDSGHIIVPGIYDEVVPLTEEBINTYKAIHL 315
QY 317 DLBEYNSRREVEKFLPDTYKEIILMLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
DB 316 DLBEYNSRREVEKFLPDTYKEIILMLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375
QY 377 RLVPNNVSAVEKQVTRHLEDVFSKRNSSNKQVSMTLGLHPWIANIDTQYLAARAIR 436

DB 376 RLVPNNVSAVEKQVTRHLEDVFSKRNSSNKQVSMTLGLHPWIANIDTQYLAARAIR 435
QY 437 TVFGTEPDMIRDSGTIPAKMFOEIVHGSVYLIPGAVDDGESHQNEKINRNNYIEGTYL 496
DB 436 TVFGTEPDMIRDSGTIPAKMFOEIVHGSVYLIPGAVDDGESHQNEKINRNNYIEGTYL 495
QY 497 FAAPFLEMAQLH 508
DB 496 FAAPFLEMAQLH 507
RESULT 12
ID ABO19431
ABO19431 standard; protein; 507 AA.
AC ABO19431;
XX
XX 27-AUG-2003 (first entry)
DT
XX
XX Human secreted / transmembrane polypeptide PRO4380.
DE
XX
XX Human; gene therapy; diabetes; obesity; hypoinsulinaemia.
KW Homo sapiens.
OS
XX
XX US2003027249-A1.
PN
XX
XX 06-FEB-2003.
PD
XX
XX 16-AUG-2001; 2001US-00931836.
PF
XX
XX 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129123P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 14-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005841.
PR 22-MAY-2000; 2000MO-US014042.
PR 02-JUN-2000; 2000MO-US015264.
PR 22-AUG-2000; 2000US-0064848.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 01-JUN-2001; 2001US-00854280.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001US-00869599.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Deenoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-492030/46.
 DR N-PSDB; ACD28837.
 XX
 PT New isolated, secreted and transmembrane PRO polypeptides and encoding
 PT nucleic acids, useful for the diagnosis and treatment of disorders such
 PT as diabetes, obesity and/or hypoinsulinemia.
 XX
 PS Claim 12; Fig 26; 196pp; English.
 XX
 CC The invention relates to a new isolated nucleic acid which encodes a PRO
 CC polypeptide. The methods and compositions of the present invention are
 CC useful for the diagnosis and treatment of disorders associated with the
 CC PRO polypeptides, such as diabetes, obesity and hypoinsulinemia. The
 CC present sequence represents the amino acid sequence of a human secreted
 CC and transmembrane PRO polypeptide
 CC
 XX Sequence 507 AA;
 SQ
 Query Match 96.9%; Score 492; DB 6; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 LLLLEKGMFSSPPPALLEKVFQYIDLHDEFEVQIKEMVAIESDSVQPPRRQELF 76
 DB 16 LLLLEKGMFSSPPPALLEKVFQYIDLHDEFEVQIKEMVAIESDSVQPPRRQELF 75
 QY 77 RMAVAADTLQRLGARVASVDMGPOQLPDGSLPIPVITLAEIGSDPTKGVCFYGHLDV 136
 DB 76 RMAVAADTLQRLGARVASVDMGPOQLPDGSLPIPVITLAEIGSDPTKGVCFYGHLDV 135
 QY 137 QPADRGGMWLTDPVYLTEVDGKLYGRGATDNKGPVLAMINAVAFRLAEODLPVNIKFII 196
 DB 136 QPADRGGMWLTDPVYLTEVDGKLYGRGATDNKGPVLAMINAVAFRLAEODLPVNIKFII 195
 QY 197 EGMEEAGSVALLEIVEKEKORFFSGVDYIVISDNLMISQKKPAITYTGRGNSYFMEVVKC 256
 DB 196 EGMEEAGSVALLEIVEKEKORFFSGVDYIVISDNLMISQKKPAITYTGRGNSYFMEVVKC 255
 QY 257 RDODFHSGTGGTILHEPMADLVALGSLVDSSGIIIVPGIYDEVVPLTEEBINYYKAIHL 316
 DB 256 RDODFHSGTGGTILHEPMADLVALGSLVDSSGIIIVPGIYDEVVPLTEEBINYYKAIHL 315
 QY 317 DLEBYRASSRVEKFLPTKEEILMLWRYPISLHIGIEGAFDEPGTKTVIPGRVIGKFSI 376
 DB 316 DLEBYRASSRVEKFLPTKEEILMLWRYPISLHIGIEGAFDEPGTKTVIPGRVIGKFSI 375
 QY 377 RLYVPHNVSAYEKOVTNLEEDVPSKRNSSNMVSVMTLGLHPWTANIDTQYLAAKAIR 436
 DB 376 RLYVPHNVSAYEKOVTNLEEDVPSKRNSSNMVSVMTLGLHPWTANIDTQYLAAKAIR 435
 QY 437 TVEGTEEDMTLDGSGTILPAKFOEIVHKSVTLPLGAVDOSEHONKIKRMNYIEGTKL 496
 DB 436 TVEGTEEDMTLDGSGTILPAKFOEIVHKSVTLPLGAVDOSEHONKIKRMNYIEGTKL 495
 QY 497 FAAFLEMAQLH 508

DB 496 FAAFLEMAQLH 507
 |||||
 RESULT 13
 ID ABU69092 standard; protein; 507 AA.
 XX
 AC ABU69092;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #13.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein; cancer;
 KW non-insulin dependent diabetes mellitus; septic shock; stroke;
 KW rheumatoid arthritis; graft-versus-host disease; cardiac ischemia;
 KW psoriasis; inflammatory bowel disease; asthma; antidiabetic; cytostatic;
 KW immunosuppressive; antineoplastic; antiarthritic; cerebroprotective;
 KW vasotropic; antipeptidic; antiinflammatory; antiaesthetic.
 XX
 OS Homo sapiens.
 XX
 PN US2003008348-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 26-DEC-2001; 2001US-00035855.
 XX
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 22-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 23-DEC-1998; 98US-011440P.
 PR 12-JAN-1999; 98US-0115552P.
 PR 22-JAN-1999; 98US-0116643P.
 PR 23-MAR-1999; 98US-0125774P.
 PR 23-MAR-1999; 98US-0125778P.
 PR 24-MAR-1999; 98US-0125826P.
 PR 31-MAR-1999; 98US-0127035P.
 PR 05-APR-1999; 98US-012706P.
 PR 13-APR-1999; 98US-0129122P.
 PR 21-APR-1999; 98US-0130359P.
 PR 27-APR-1999; 98US-0131270P.
 PR 27-APR-1999; 98US-0131272P.
 PR 27-APR-1999; 98US-0131272P.
 PR 27-APR-1999; 98US-0131272P.
 PR 04-MAY-1999; 98US-0132371P.
 PR 04-MAY-1999; 98US-0132379P.
 PR 04-MAY-1999; 98US-0132383P.
 PR 14-MAY-1999; 98US-0132383P.
 PR 25-MAY-1999; 98US-0135750P.
 PR 08-JUN-1999; 98US-0138166P.
 PR 20-JUL-1999; 98US-0144791P.
 PR 03-AUG-1999; 98US-0146970P.
 PR 29-OCT-1999; 98US-0162506P.
 PR 02-DEC-1999; 98US-0162506P.
 PR 22-DEC-1999; 98US-0162506P.
 PR 01-MAR-2000; 98US-0162506P.
 PR 02-MAR-2000; 98US-0162506P.
 PR 22-MAY-2000; 98US-0162506P.
 PR 02-JUN-2000; 98US-0162506P.
 PR 23-AUG-2000; 98US-0162506P.
 PR 24-AUG-2000; 98US-0162506P.
 PR 01-DEC-2000; 98US-0162506P.
 PR 20-DEC-2000; 98US-0162506P.
 PR 28-FEB-2001; 98US-0162506P.
 PR 01-JUN-2001; 98US-0162506P.
 PR 20-JUN-2001; 98US-0162506P.
 PR 29-JUN-2001; 98US-0162506P.
 PR 09-JUL-2001; 98US-0162506P.
 PR 16-AUG-2001; 98US-0162506P.

XX (GETH) GENENTECH INC.
PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,
PI Stewart TA, Matanabe CK, Wood WI, Zhang Z;
XX WPI, 2003-341326/32.
DR N-PSDB; ACAd0111.
XX
XX New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
PT treating diabetes mellitus, cancers, septic shock, inflammatory bowel
PT disease or asthma, or in gene therapy, chromosome identification or
PT tissue typing.
PS Claim 12; Fig 26; 196pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or treating non
CC -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
CC arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
CC psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
CC sequences may be used as hybridisation probes in chromosome and gene
CC mapping, or in generating antisense RNA and DNA. They are also useful in
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, to generate transgenic animals or
CC knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification, and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO polypeptides, or for the affinity
CC purification of the polypeptides from recombinant cell culture or natural
CC sources. ABU6980-ABU69102 represent the human PRO polypeptides of the
CC invention
CC
SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 6; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLERGMFSSPPSPALLLEKVFQYIDIHODEFVTLKEMVAIESDSVQVPRFQELF 76
DB 16 LLLLLERGMFSSPPSPALLLEKVFQYIDIHODEFVTLKEMVAIESDSVQVPRFQELF 75
QY 77 RMAVAADTLQRLGAVASVDMGPQOLPDGQSLPFPVLLAELGSDPTGTGTCFQHLDV 136
DB 76 RMAVAADTLQRLGAVASVDMGPQOLPDGQSLPFPVLLAELGSDPTGTGTCFQHLDV 135
QY 137 QPADRGDGLTDPYVLTVEYDGLYGRGATDNKGPVLAWINAVSAFRLBQDLPVNIKFI 196
DB 136 QPADRGDGLTDPYVLTVEYDGLYGRGATDNKGPVLAWINAVSAFRLBQDLPVNIKFI 195
QY 197 EGMERAGSYALBELVEKEKORFPGVDYIVISDNLMISQRKPAITYTGSGNSYFMWEVXC 256
DB 196 EGMERAGSYALBELVEKEKORFPGVDYIVISDNLMISQRKPAITYTGSGNSYFMWEVXC 255
QY 257 RRODFFSGTGGIIEHPMADLVALLGSIVDSSGHILVPIYEVVPLEEBEINTYKALHL 316
DB 256 RRODFFSGTGGIIEHPMADLVALLGSIVDSSGHILVPIYEVVPLEEBEINTYKALHL 315
QY 317 DLEBYRNSRVEKFLFDTKEEILMLMRYPSTLSIHGIEGAPDEPGKTVIPGVIGKFSI 376
DB 316 DLEBYRNSRVEKFLFDTKEEILMLMRYPSTLSIHGIEGAPDEPGKTVIPGVIGKFSI 375
QY 377 RLVPHNVAVAEKOYTRHLEDVFSKRNSSNKRVVSWTGLAFWIANIDDTQYLAARLR 436
DB 376 RLVPHNVAVAEKOYTRHLEDVFSKRNSSNKRVVSWTGLAFWIANIDDTQYLAARLR 435
QY 437 TVFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNIIEGTYL 496
DB 437 TVFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNIIEGTYL 496

DB 436 TVFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNIIEGTYL 495
QY 497 PAAFFLEMAQLH 508
DB 496 PAAFFLEMAQLH 507

RESULT 14
ABU81556
ID ABU81556 standard; protein; 507 AA.
XX
AC ABU81556;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human secreted polypeptide PRO4380.
XX
KW Human; inflammatory disease; organ failure; atherosclerosis; cancer;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW differential disorder; cell adhesion disorder; skin disorder;
KW neural receptor disorder; diabetic complication; tissue typing.
XX
OS Homo sapiens.
XX
PN US2002192751-A1.
XX
PD 19-DEC-2002.
XX
PF 26-DEC-2001; 2001US-00036041.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 22-JAN-1999; 99US-0115552P.
PR 12-JAN-1999; 99US-0116843P.
PR 22-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125828P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 15-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-0162506P.
PR 22-DEC-1999; 99US-0162506P.
PR 01-MAR-2000; 2000US-0005601.
PR 02-MAR-2000; 2000US-0005601.
PR 22-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0015264.
PR 23-AUG-2000; 2000US-0023522.
PR 24-AUG-2000; 2000US-0023328.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 01-JUN-2001; 2001US-0017800.
PR 20-JUN-2001; 2001US-0019682.
PR 29-JUN-2001; 2001US-0021086.
PR 09-JUL-2001; 2001US-0021735.

PR 16-AUG-2001; 2001US-00931836.
 XX (GETH) GENENTECH INC.
 XX
 PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-341079/32.
 XX N-PSDB; ACA67734.
 DR
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.
 XX
 XX
 PS Claim 12; Fig 26; 195pp; English.
 XX
 CC The invention relates to an isolated nucleic acid that encodes a PRO
 CC polypeptide. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, acquired immunodeficiency
 CC syndrome (AIDS), cancer, differentiation disorders, cell adhesion
 CC disorders, neural receptor disorders, skin disorders or diabetic
 CC complications. The nucleic acids are useful as hybridisation probes, in
 CC chromosome and gene mapping and in generating antisense RNA or DNA. The
 CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
 CC bioreactors. Both are useful in tissue typing. The present sequence
 CC represents the amino acid sequence of a PRO polypeptide of the invention
 XX
 XX Sequence 507 AA;

Query Match 96.9%; Score 492; DB 6; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLLGGSSSSPPALLKKVFOYIDLHODEFVQTLKEMVAIESDSVQVPRFRQELF 76
 DB 16 LLLLLLGGSSSSPPALLKKVFOYIDLHODEFVQTLKEMVAIESDSVQVPRFRQELF 75
 QY 77 RMAVAADTLQRLGARAVADMGPPQQLPDGQSLPIPVVILAEIGSDPTKGTVCYGHLDV 136
 DB 76 RMAVAADTLQRLGARAVADMGPPQQLPDGQSLPIPVVILAEIGSDPTKGTVCYGHLDV 135
 QY 137 QPADRDGMLTDYVLTENVGKLYGRGATDNKGPVLAMINAVSAFRLBDLPVNIKEFI 196
 DB 136 QPADRDGMLTDYVLTENVGKLYGRGATDNKGPVLAMINAVSAFRLBDLPVNIKEFI 195
 QY 197 EGMEEAGSVALLEELVEKEKDRPFSGVDYIISDNLWISQKPAITYGTRGNSYFMVEYKC 256
 DB 196 EGMEEAGSVALLEELVEKEKDRPFSGVDYIISDNLWISQKPAITYGTRGNSYFMVEYKC 255
 QY 257 RODDFHSCTGGGILHBMADVLALLGLSDSSGHILVPGYIDVAVPLTEEEINTYQAHL 316
 DB 256 RODDFHSCTGGGILHBMADVLALLGLSDSSGHILVPGYIDVAVPLTEEEINTYQAHL 315
 QY 317 DLEBYNNSRVEKEFLPTKEEILMHLWRYPSSLIHIGIEGAFDEPGTKTVPGRVIKFSI 376
 DB 316 DLEBYNNSRVEKEFLPTKEEILMHLWRYPSSLIHIGIEGAFDEPGTKTVPGRVIKFSI 375
 QY 377 RLVPHANVSAVEKQVTRHLEDVFSKNSNKNVSMVMTGLHPVIANIDTQYLAARAIR 436
 DB 376 RLVPHANVSAVEKQVTRHLEDVFSKNSNKNVSMVMTGLHPVIANIDTQYLAARAIR 435
 QY 437 TVGTEPDMIRDSSTPIAMPEIYHKSYYVILPLGAVDDGESHQNEKINRMVYIGSTKL 496
 DB 436 TVGTEPDMIRDSSTPIAMPEIYHKSYYVILPLGAVDDGESHQNEKINRMVYIGSTKL 495
 QY 497 FAFPLEMAQLH 508
 DB 496 FAFPLEMAQLH 507

RESULT 15

ADA76582
 ID ADA76582 standard; protein; 507 AA.
 XX
 AC ADA76582;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO4380.
 XX
 KW human; secreted and transmembrane protein; PRO; tumour; gene therapy;
 KW tissue typing; chromosome identification; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003036114-A1.
 XX
 XX 20-FEB-2003.
 PD
 XX
 PF 26-DEC-2001; 2001US-00035719.
 XX
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 22-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 23-DEC-1998; 98US-0114140P.
 PR 12-JAN-1999; 98US-0115552P.
 PR 22-JAN-1999; 98US-0116843P.
 PR 23-MAR-1999; 98US-0125774P.
 PR 23-MAR-1999; 98US-0125778P.
 PR 24-MAR-1999; 98US-0125826P.
 PR 31-MAR-1999; 98US-0127035P.
 PR 05-APR-1999; 98US-0127706P.
 PR 13-APR-1999; 98US-0129122P.
 PR 21-APR-1999; 98US-0130359P.
 PR 27-APR-1999; 98US-0131270P.
 PR 27-APR-1999; 98US-0131272P.
 PR 27-APR-1999; 98US-0131291P.
 PR 04-MAY-1999; 98US-0132371P.
 PR 04-MAY-1999; 98US-0132379P.
 PR 04-MAY-1999; 98US-0132383P.
 PR 14-MAY-1999; 98US-0135703P.
 PR 25-MAY-1999; 98US-0135750P.
 PR 08-JUN-1999; 98US-0138166P.
 PR 20-JUL-1999; 98US-0144791P.
 PR 03-AUG-1999; 98US-0146970P.
 PR 29-OCT-1999; 98US-0162506P.
 PR 02-DEC-1999; 98US-02028551.
 PR 22-DEC-1999; 98US-0307720.
 PR 01-MAR-2000; 2000US-005601.
 PR 02-MAR-2000; 2000US-005841.
 PR 22-MAY-2000; 2000US-014042.
 PR 02-JUN-2000; 2000US-015264.
 PR 23-AUG-2000; 2000US-023322.
 PR 24-AUG-2000; 2000US-023328.
 PR 01-DEC-2000; 2000US-023678.
 PR 20-DEC-2000; 2000US-023956.
 PR 28-FEB-2001; 2001US-0006520.
 PR 01-JUN-2001; 2001US-0178800.
 PR 20-JUN-2001; 2001US-019692.
 PR 29-JUN-2001; 2001US-02021066.
 PR 09-JUL-2001; 2001US-02021735.
 PR 16-AUG-2001; 2001US-00931836.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-615764/58.
 XX N-PSDB; ADA76581.
 XX

PT Novel isolated secreted and transmembrane polypeptides, designated as PRO
PT polypeptides e.g. PRO434, PRO434 and PRO1122, useful for inhibiting
PT tumor cell growth, and for preparing medicaments for therapeutic use.
XX
XX
PS Claim 12; Fig 26; 201pp; English.

CC The invention describes an isolated secreted and transmembrane PRO
CC polypeptide (I), having at least 80% identity to or scoring at least 80%
CC positives when compared to, a sequence (S1) comprising 246, 440, 197, 97,
CC 273, 571, 209, 888, 502, 310, 251, 800, 507, 248, 223, 134, 136, 468,
CC 328, 221, 194, 899, or 339 amino acids fully defined in the
CC specification. An anti-(I)-antibody is useful for determining the
CC presence of (I) in a cell. (I) is useful for identifying a compound
CC capable of inhibiting the expression and/or activity of (I). (I) and the
CC antibody are useful for inhibiting the growth of tumour cells, and for
CC the preparation of a medicament useful in the treatment of a condition
CC which is responsive to (I) or the antibody. A polynucleotide (II)
CC encoding (I) is also useful for isolating full-length PRO cDNA for
CC generating transgenic animals or knock-out animals, which are, in turn,
CC are useful in the development in the screening of therapeutically useful
CC reagents, and in gene therapy. PRO is useful in assays to identify other
CC proteins or molecules involved in binding interactions, for screening
CC inhibitors or agonists of binding interactions and for screening chemical
CC libraries. (I) is useful as molecular weight marker for protein
CC electrophoresis, and as therapeutic agents. (I) or (II) is useful for
CC tissue typing and for chromosome identification. Ab is useful in
CC diagnostic assays for PRO, in affinity purification of PRO, and for
CC detection of PRO in biological samples. This is the amino acid sequence
CC of a novel human secreted and transmembrane PRO polypeptide.
XX
XX

SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 6; Length 507;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLEERGFSSPPALLLEKVFQYIDHODEFVQTLKEWAIESDSVQVPRRQBLE 76
DB 16 LLLLEERGFSSPPALLLEKVFQYIDHODEFVQTLKEWAIESDSVQVPRRQBLE 75
QY 77 RMAVAADTLORLGAVASVDMGPOOLPGOSLPFPVTLAEGSDPTKGVCFGHLDV 136
DB 76 RMAVAADTLORLGAVASVDMGPOOLPGOSLPFPVTLAEGSDPTKGVCFGHLDV 135
QY 137 QPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPVNIKEFI 196
DB 136 QPADRGDGLTDPYVLTVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPVNIKEFI 195
QY 197 EGMERAGSVALBELVEKEKORFPSCVDYVVISDNLMISQRKALITYGRGNSYFMEVVC 256
DB 196 EGMERAGSVALBELVEKEKORFPSCVDYVVISDNLMISQRKALITYGRGNSYFMEVVC 255
QY 257 RODPHSGTFFGILHEPMADVALLGSIVDSGHILVPGIYEVVPLTEETINTKATHL 316
DB 256 RODPHSGTFFGILHEPMADVALLGSIVDSGHILVPGIYEVVPLTEETINTKATHL 315
QY 317 DLEERYNRSRVEKFLPDTKEEILMLMRYSLSIHIGEGAFDEPGTKVTPRVIGKFSI 376
DB 316 DLEERYNRSRVEKFLPDTKEEILMLMRYSLSIHIGEGAFDEPGTKVTPRVIGKFSI 375
QY 377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSKNVSVMTGLAFHWIANIDDTQYLAARAIR 436
DB 376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSKNVSVMTGLAFHWIANIDDTQYLAARAIR 435
QY 437 TVFGTEPDMIRBGSITPIAKMFOEIVHKSIVLIPGAVDDGSHSONEKINRNRYEGTKL 496
DB 436 TVFGTEPDMIRBGSITPIAKMFOEIVHKSIVLIPGAVDDGSHSONEKINRNRYEGTKL 495
QY 497 FAAPFLEMAQLH 508
DB 496 FAAPFLEMAQLH 507

RESULT 16
ABO25139
ID ABO25139 standard; protein; 507 AA.
XX
XX
AC ABO25139;
XX
DT 05-SEP-2003 (first entry)
XX
XX
DE Human secreted/transmembrane protein PRO4380.
XX
XX
KW Human; PRO; secreted protein; transmembrane protein; septic shock;
XX gene therapy.
XX
OS Homo sapiens.
XX
PN US2003044842-A1.
PD
XX
XX 06-MAR-2003.
PF
XX 26-DEC-2001; 2001US-00036160.
XX
XX 15-MAY-1998; 98US-0098579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 98US-0115552P.
PR 22-JAN-1999; 98US-0116843P.
PR 23-MAR-1999; 98US-0125774P.
PR 23-MAR-1999; 98US-0125778P.
PR 24-MAR-1999; 98US-0125826P.
PR 31-MAR-1999; 98US-0127035P.
PR 05-APR-1999; 98US-0127706P.
PR 13-APR-1999; 98US-0128122P.
PR 21-APR-1999; 98US-0130359P.
PR 27-APR-1999; 98US-0131270P.
PR 27-APR-1999; 98US-0131272P.
PR 27-APR-1999; 98US-0131291P.
PR 04-MAY-1999; 98US-0132371P.
PR 04-MAY-1999; 98US-0132379P.
PR 04-MAY-1999; 98US-0132383P.
PR 14-MAY-1999; 98US-0132383P.
PR 25-MAY-1999; 98US-0135750P.
PR 08-JUN-1999; 98US-0138166P.
PR 20-JUL-1999; 98US-0144791P.
PR 03-AUG-1999; 98US-0146970P.
PR 29-OCT-1999; 98US-0162506P.
PR 02-DEC-1999; 98US-0162506P.
PR 22-DEC-1999; 98US-0162506P.
PR 01-MAR-2000; 2000US-0005601.
PR 02-MAR-2000; 2000US-0005601.
PR 22-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0015264.
PR 23-AUG-2000; 2000US-0023522.
PR 24-AUG-2000; 2000US-0023522.
PR 01-DEC-2000; 2000US-0023522.
PR 20-DEC-2000; 2000US-0023522.
PR 20-FEB-2001; 2001US-0006520.
PR 01-JUN-2001; 2001US-0017800.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 16-AUG-2001; 2001US-00931836.
XX
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-492260/46.
DR N-PSDB; ACD42296.

23-DEC-1998; 99US-0114140P.
PR
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0133291P.
PR 04-MAY-1999; 99US-0133371P.
PR 04-MAY-1999; 99US-0132379P.
PR 14-MAY-1999; 99US-0132383P.
PR 25-MAY-1999; 99WO-US010733.
PR 08-JUN-1999; 99US-0135750P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US036278.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.

(GETH) GENENTECH INC.

XX PA Deenoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,
XX PI Stewart TA, Watanabe CK, Wood WT, Zhang Z;
XX N-PSDB; AAD59362.

XX WP1; 2003-585109/55.

DR DR N-PSDB; AAD59362.

XX PT New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT acids, useful for diagnosing, preventing and/or treating inflammation,
PT nephropathies, bone and cartilage disorders, and diabetes.
XX XX

PS Claim 12; Fig 26; 203pp; English.

XX The invention relates to an isolated nucleic acid that encodes a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for the diagnosis, prevention and/or treatment of inflammation,
CC nephropathies, bone and cartilage disorders, such as arthritis and
CC disorders that affect glucose or free fatty acid (FFA) uptake, such as
CC diabetes, hypoparathyroidism or hyperparathyroidism. The PRO polypeptides are
CC also useful as molecular weight markers or for chromosome identification.
CC The PRO genes are useful as hybridisation probes or for screening
CC libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be
CC used in gene therapy and anticancer therapy. The present sequence is human
CC PRO protein.

XQ Sequence 507 AA;

Query Match	96.9%	Score 492	DB 7	Length 507
Best Local Similarity	100.0%	Pred. No. 0		
Matches 492, Conservative 0, Mismatches 0, Indels 0, Gaps 0,				
17 LLLLLRRMSSSSPPPALAKRYIILHDDFQITLKENVAISDSVQVPRRQELF				76

Db	16	LIILLLEKGMSSSPSPALLKPKYQYIIDLHODEFVOTLKEMWALIESDSVQVPRRRQELF	75
Qy	77	RMAVAADDTQRLGARVASVDMGPQQLPDGQSLIPBPVILAEIGSDPTKGVCFYGHLDV	13
Db	76	RMAVAADDTQRLGARVASVDMGPQQLPDGQSLIPBPVILAEIGSDPTKGVCFYGHLDV	13
Qy	137	QPADRGGMWLTDPVLTENVGKLYGHGATDNKGPTLAWTNAVASAPRALBODLPVNIKFTI	19
Db	136	QPADRGGMWLTDPVLTENVGKLYGHGATDNKGPTLAWTNAVASAPRALBODLPVNIKFTI	19
Qy	197	EGMEEAGSVALBEELVEKEKDRFPFSGVDYIVISDNLWISQRKPAITYTGRKNSYFMWEVKC	25
Db	196	EGMEEAGSVALBEELVEKEKDRFPFSGVDYIVISDNLWISQRKPAITYTGRKNSYFMWEVKC	25
Qy	257	RDDQFHSGTGGTGLIHPMADVLALGSLVDSGSHLVPGIYDVPVPLTBEELINTYKAIHL	31
Db	256	RDDQFHSGTGGTGLIHPMADVLALGSLVDSGSHLVPGIYDVPVPLTBEELINTYKAIHL	31
Qy	317	DLEBYRNSRVEKEFLPTKEEILMLHMRPSSLIHGIEGAPDEPGKTVIPGRVIGKFSI	37
Db	316	DLEBYRNSRVEKEFLPTKEEILMLHMRPSSLIHGIEGAPDEPGKTVIPGRVIGKFSI	37
Qy	437	TVGTSTEDMDIRDSSTPIAKMPEIYHKRVVLIPGAVDDGSHSQNEKINRMNTEGKL	49
Db	436	TVGTSTEDMDIRDSSTPIAKMPEIYHKRVVLIPGAVDDGSHSQNEKINRMNTEGKL	49
Qy	497	FAAFLEMAQLH 508	
Db	496	FAAFLEMAQLH 507	
RESULT 18			
AAE39046	ID	AAE39046 standard; protein; 507 AA.	
XX	AC	AAE39046;	
XX	DE	18-DEC-2003 (first entry)	
XX	XX	Human PRO4380 protein.	
XX	KW	Human; diagnosis; inflammation; nephropathy; bone disorder; arthritis;	
XX	KW	cartilage disorder; hypoinulinaemia; hyperinsulinaemia; gene therapy;	
XX	KW	antisenese therapy; diabetes; PRO.	
OS	XX	Homo sapiens.	
XX	XX		
FT	FT	Key	Location/Qualifiers
FT	FT	Peptide	1..26
FT	FT	Protein	/label= Signal_peptide
FT	FT	Modified-site	27..507
FT	FT	Modified-site	/note= "Mature human PRO protein"
FT	FT	Modified-site	89..95
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	119..125
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	140..143
FT	FT	Modified-site	/note= "Cell attachment sequence"
FT	FT	Region	156..167
FT	FT	Modified-site	/note= "ArgE/dapE/ACYI/CPG"
FT	FT	Modified-site	162..168
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	197..203
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	242..248
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	263..269
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Domain	273..292

KW tissue typing; chromosome identification; gene therapy;
 KW chromosome mapping; gene mapping; sports injury; arthritis; diabetes;
 KW obesity; hyper-insulinaemia; hypo-insulinaemia; thalassemia;
 KW Berger disease; Schonlein-Henoch purpura; celiac disease;
 KW dermatitis herpetiformis; Crohn's disease.

OS Homo sapiens.

XX US2003092063-A1.

XX 15-MAY-2003.

PF 26-DEC-2001; 2001US-00036063.

XX 15-MAY-1998; 98US-0085579P.

PR 15-DEC-1998; 98US-0112514P.

PR 22-DEC-1998; 98US-0113300P.

PR 23-DEC-1998; 98US-0113430P.

PR 23-DEC-1998; 98US-0113605P.

PR 23-DEC-1998; 98US-0114140P.

PR 12-JAN-1999; 99US-0115552P.

PR 22-JAN-1999; 99US-0116843P.

PR 23-MAR-1999; 99US-0125774P.

PR 23-MAR-1999; 99US-0125778P.

PR 31-MAR-1999; 99US-0125826P.

PR 05-APR-1999; 99US-0127035P.

PR 13-APR-1999; 99US-0127066P.

PR 21-APR-1999; 99US-0130359P.

PR 27-APR-1999; 99US-0131270P.

PR 27-APR-1999; 99US-0131272P.

PR 04-MAY-1999; 99US-0132371P.

PR 04-MAY-1999; 99US-0132379P.

PR 14-MAY-1999; 99US-0132833P.

PR 25-MAY-1999; 99US-0135750P.

PR 08-JUN-1999; 99US-0138166P.

PR 20-JUL-1999; 99US-0144791P.

PR 03-AUG-1999; 99US-0146970P.

PR 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99US-01628551.

PR 22-DEC-1999; 99US-01628551.

PR 01-MAR-2000; 2000US-0005601.

PR 02-MAR-2000; 2000US-0005841.

PR 22-MAY-2000; 2000US-0014042.

PR 02-JUN-2000; 2000US-0015264.

PR 23-AUG-2000; 2000US-0023522.

PR 24-AUG-2000; 2000US-0023328.

PR 01-DEC-2000; 2000US-0034678.

CC The invention describes an isolated secreted and transmembrane PRO
 CC polypeptide (i) having at least 80% amino acid sequence identity to fully
 CC defined sequences of 246, 440, 197, 97, 273, 571, 209, 888, 502, 310,
 CC 251, 800, 507, 248, 223, 134, 136, 468, 322, 221, 194, 125 or 339 amino
 CC acids as given in the specification. (i) is useful for tissue typing, as
 CC molecular weight markers or as therapeutic agents. A polynucleotide (ii)
 CC encoding (i) is useful for chromosome identification, gene therapy,
 CC tissue typing or as hybridisation probes in chromosome and gene mapping.
 CC PRO1484, PRO1890, PRO1887, PRO4357, PRO4357, PRO4405, PRO5737 and PRO5990
 CC is useful for treating sports injuries and arthritis. PRO1484, PRO1122,
 CC PRO1889, PRO4357, PRO4380 and PRO4356 are useful for treating diabetes.
 CC PRO4334, PRO4425, PRO4425, PRO4430, PRO1890, PRO1785 and PRO4422 are
 CC useful for treating obesity, diabetes or hyper- or hypo-insulinaemia.
 CC PRO4352, PRO4354, PRO4408, PRO6030 and PRO4499 are useful for treating
 CC thalassemia. PRO4380, PRO4408 and PRO4425 are useful for treating Berger
 CC disease, Schonlein-Henoch purpura, celiac disease, dermatitis
 CC herpetiformis or Crohn's disease. This is the amino acid sequence of a
 CC novel human secreted and transmembrane PRO polypeptide.

CC Sequence 507 AA;

Query Match 96.9%; Score 492; DB 7; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLEKGFSSPPPALLEKVFQYIDHODEFYQTLKEMWYISDSQVPRPROELF 76
 Db 16 LLLLEKGFSSPPPALLEKVFQYIDHODEFYQTLKEMWYISDSQVPRPROELF 75
 QY 77 RMMVAADTLQRLGARVASVDMKPDQSLPIPIVYLAELSGDPTKGTVCYGHLDV 136
 Db 76 RMMVAADTLQRLGARVASVDMKPDQSLPIPIVYLAELSGDPTKGTVCYGHLDV 135
 QY 137 QPADRGDMLTDPVYLTVDGKLYGRGATDKNGPLATINVASARALEQDLPNVTKPII 196
 Db 136 QPADRGDMLTDPVYLTVDGKLYGRGATDKNGPLATINVASARALEQDLPNVTKPII 195
 QY 197 EGMERAGSVALEELVEKEKORFFSGVDYIYSDNMIQORPATYTGTRGNSYFVWEVC 256
 Db 196 EGMERAGSVALEELVEKEKORFFSGVDYIYSDNMIQORPATYTGTRGNSYFVWEVC 255
 QY 257 RDQDFHSGTFGGIILHEPMADLVALLGSLVDSGGHILVGVYDEVVPLTEBEINTYKAIHL 316
 Db 256 RDQDFHSGTFGGIILHEPMADLVALLGSLVDSGGHILVGVYDEVVPLTEBEINTYKAIHL 315
 QY 317 DLEERYNSRVEKLEFQKEELIMLMWYPSLSIHGIGADEPCTKVIPIGVGKESI 376
 Db 316 DLEERYNSRVEKLEFQKEELIMLMWYPSLSIHGIGADEPCTKVIPIGVGKESI 375
 QY 377 RLVPHMANSAYEKQVTRHLEDVFSKRNSNKMVSMTGILHPWIANIDTOYLAARAIIR 436
 Db 376 RLVPHMANSAYEKQVTRHLEDVFSKRNSNKMVSMTGILHPWIANIDTOYLAARAIIR 435
 QY 437 TVFGTEPMDIRDSSTPIAKMFOEIVHKSIVLIPGAVDDGSHSQNEKINRWNYEGTKL 496
 Db 436 TVFGTEPMDIRDSSTPIAKMFOEIVHKSIVLIPGAVDDGSHSQNEKINRWNYEGTKL 495
 QY 497 FAAPFLEMAQLH 508
 Db 496 FAAPFLEMAQLH 507

RESULT 20
 ADF09256 standard; protein; 507 AA.

XX ADF09256;

AC 12-FEB-2004 (first entry)

DE Human secreted and transmembrane protein PRO4380.

XX cytosolic; gene therapy; human; secreted and transmembrane; PRO; cancer;

XX	tumour;chromosome mapping; gene mapping; therapeutic reagent.
OS	Homo sapiens.
NN	US2003134327-A1.
XX	17-JUL-2003.
PD	
XX	26-DEC-2001, 2001US-00035977.
XX	
PR	15-MAY-1998; 98US-0085579P.
PR	15-DEC-1998; 98US-0112514P.
PR	22-DEC-1998; 98US-0113300P.
PR	23-DEC-1998; 98US-0113430P.
PR	23-DEC-1998; 98US-0113605P.
PR	23-DEC-1998; 98US-0113621P.
PR	12-JAN-1999; 99US-0115552P.
PR	22-JAN-1999; 99US-0116842P.
PR	23-MAR-1999; 99US-0125774P.
PR	24-MAR-1999; 99US-0125789P.
PR	24-MAR-1999; 99US-0125826P.
PR	31-MAR-1999; 99US-0127033P.
PR	05-APR-1999; 99US-0127706P.
PR	13-APR-1999; 99US-0129122P.
PR	21-APR-1999; 99US-0130359P.
PR	27-APR-1999; 99US-0131270P.
PR	27-APR-1999; 99US-0131279P.
PR	27-APR-1999; 99US-0131291P.
PR	04-MAY-1999; 99US-0132371P.
PR	04-MAY-1999; 99US-0132379P.
PR	04-MAY-1999; 99US-0132383P.
PR	14-MAY-1999; 99WO-US010733.
PR	25-MAY-1999; 99WO-US013570P.
PR	08-JUN-1999; 99US-0138166P.
PR	20-JUL-1999; 99US-0144792P.
PR	03-AUG-1999; 99US-0146970P.
PR	29-OCT-1999; 99US-0162506P.
PR	02-DEC-1999; 99WO-US028551.
PR	22-DEC-1999; 99WO-US030770.
PR	01-MAR-2000; 2000WO-US005601.
PR	02-MAR-2000; 2000WO-US005841.
PR	22-MAY-2000; 2000WO-US014042.
PR	02-JUN-2000; 2000WO-US015264.
PR	23-AUG-2000; 2000WO-US023522.
PR	24-AUG-2000; 2000WO-US023338.
PR	01-DEC-2000; 2000WO-US032478.
PR	20-DEC-2000; 2000WO-US034956.
PR	28-FEB-2001; 2001WO-US006550.
PR	01-JUN-2001; 2001WO-US017800.
PR	20-JUN-2001; 2001WO-US019692.
PR	09-JUL-2001; 2001WO-US021066.
PR	16-AUG-2001; 2001US-00931836.
XX	
XX	(GETH) GENENTECH INC.
PA	
PI	Deanyers L, Eaton DL, Goddard A, Godowski P, Gurney AL, Pan J;
PI	Stewart TA, Watanabe CK, Wood WL, Zhang Z;
XX	
DR	WPI; 2004-031325/03.
DR	N-PSDB; ADFO9255.
XX	
PT	Twenty three nucleic acids encoding PRO polypeptides, useful in
PT	chromosome and gene mapping, in generating antisense RNA and DNA and in
XX	gene therapy.
XX	
PS	Claim 12; SEQ ID NO 57; 261pp; English.
CC	The invention describes 23 nucleic acids encoding human secreted and
CC	transmembrane PRO polypeptides. The PRO polypeptides and nucleic acids
CC	are useful for the therapeutic treatment of cancerous tumours. The PRO
CC	polynucleotide is useful in molecular biology, including uses as

CC	hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. This is the amino acid sequence of a novel human secreted and transmembrane protein PRO1484.
CC	Sequence 507 AA;
CC	Query Match 96.9%; Score 492; DB 8; Length 507;
CC	Best Local Similarity 100.0%; Pred. No. 0;
CC	Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	17 LLLLLLKGMPSSPPPALLEKVVQYIDLHODEFVQLKEWVAIESDSVQVPRFROELF 76
CC	16 LLLLLLKGMPSSPPPALLEKVVQYIDLHODEFVQLKEWVAIESDSVQVPRFROELF 75
CC	77 RMAVAADTLQRLGARVAASVDMGPOQLPDGQSLPIPVIIIAELGSDPTKCTVCYGHLDV 136
CC	76 RMAVAADTLQRLGARVAASVDMGPOQLPDGQSLPIPVIIIAELGSDPTKCTVCYGHLDV 135
CC	137 QPARGGGWLTPDVPVLTENVGKLYGRGATNKGVPVLAWINAVSAFRLLEDLPVNIKEFI 196
CC	136 QPARGGGWLTPDVPVLTENVGKLYGRGATNKGVPVLAWINAVSAFRLLEDLPVNIKEFI 195
CC	197 EGMEASGVALLLEIVEKEKRFSSGVYIYISDLWISQKKPAITYTGRGNSYPMVEVKC 256
CC	196 EGMEASGVALLLEIVEKEKRFSSGVYIYISDLWISQKKPAITYTGRGNSYPMVEVKC 255
CC	257 RDQDFSGTGGIILHEPMADLVALLGSLVDSGHIIVPGIYDEVVPLTEBEINTYKAHL 316
CC	256 RDQDFSGTGGIILHEPMADLVALLGSLVDSGHIIVPGIYDEVVPLTEBEINTYKAHL 315
CC	317 DLEIYRNSSRVEKLFPTKEEILMLHLMRYPSLSIHGIEGAFDEPGTQTVIPGRYIGFSI 376
CC	316 DLEIYRNSSRVEKLFPTKEEILMLHLMRYPSLSIHGIEGAFDEPGTQTVIPGRYIGFSI 375
CC	377 RLVEHMMVSAVEKQVTHLEDFVFSKRNSSNMKNVSMTLGLHPWTANIDDTQYLAAKRAIR 436
CC	376 RLVEHMMVSAVEKQVTHLEDFVFSKRNSSNMKNVSMTLGLHPWTANIDDTQYLAAKRAIR 435
CC	437 TVFGTEPDMIRDSGTIPDAKMFDEIVAKSVYLLPLGAVDDGEHSQNEKINRMVYIEGTKL 496
CC	436 TVFGTEPDMIRDSGTIPDAKMFDEIVAKSVYLLPLGAVDDGEHSQNEKINRMVYIEGTKL 495
CC	497 PAAFFLEMAQLH 508
CC	496 PAAFFLEMAQLH 507
CC	RESULT 21
CC	ADM12488
CC	ADM12488 standard; protein; 507 AA.
CC	ADM12488;
CC	24-MAR-2005 (first entry)
CC	Human PRO4380 protein.
CC	PRO protein; cancer; gene therapy; cytosolic; neoplasm; cell signaling; biosensor; bioreactor; photoreactor; pharmaceutical; diagnostic; PRO4380.
CC	Homo sapiens.
CC	Key Location/Qualifiers
CC	Peptide 1..26
CC	Protein 27..507
CC	Modified-site /note= "Human mature PRO4380 protein"
CC	89..95
CC	/note= "N-myristoylation site"

FT Modified-site 119. .125
 FT /note="N-myristoylation site"
 FT Region 140. .143
 FT /note="Cell attachment sequence"
 FT Region 156. .167
 FT /note="Large / daps /ACY1 / CPG "
 FT Modified-site 162. .168
 FT /note="N-myristoylation site"
 FT Modified-site 197. .203
 FT /note="N-myristoylation site"
 FT Modified-site 242. .248
 FT /note="N-myristoylation site"
 FT Modified-site 263. .269
 FT /note="N-myristoylation site"
 FT Domain 273. .292
 FT /note = Transmembrane domain
 FT Modified-site 322. .326
 FT /note="N-glycosylation site"
 FT Modified-site 351. .357
 FT /note="N-myristoylation site"
 FT Modified-site 382. .386
 FT /note="N-glycosylation site"
 FT Modified-site 400. .404
 FT /note="CAMP and cGMP-dependent protein kinase
 FT phosphorylation site"
 FT Modified-site 402. .406
 FT /note="N-glycosylation site"
 FT US2004265966-A1.
 PD 30-DEC-2004.
 XX
 XX
 XX 01-JUL-2004; 2004US-00884091.
 XX
 PF 01-MAR-2000; 2000WO-US005601.
 XX
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 16-ATG-2001; 2001US-00931836.
 XX
 XX (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURNE/) GURNEY A L.
 PA (PAN/) PAN J.
 PA (STEM/) STEWART T A.
 PA (WATA/) WATANABE C K.
 PA (WOOD/) WOOD W I.
 PA (ZHAN/) ZHANG Z.
 XX
 PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 DR N-PSDB; ADW12487.
 XX
 DR WPI; 2005-064903/07.
 XX
 PT New PRO nucleic acid or polypeptide, useful for preparing a medicament
 PT for treating a condition associated with PRO nucleic acid or polypeptide
 PT e.g., cancer.
 XX
 PS Claim 12; SEQ ID NO 57; 183pp; English.
 XX
 CC The present invention relates to a PRO proteins and their encoding
 CC nucleic acids. The invention is useful for preparing a medicament for
 CC treating a condition associated with PRO nucleic acid e.g., cancer. The
 CC invention is also useful in gene therapy. The present sequence is human
 CC PRO protein.
 XX
 SQ Sequence 507 AA;
 Query Match 96.9%; Score 492; DB 9; Length 507;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 LLLLEKGMFSSPPSPPLLEKVFQYIDLHODEFYQIKENVAIRSDSVQVPRRQELF 76
 DB 16 LLLLEKGMFSSPPSPPLLEKVFQYIDLHODEFYQIKENVAIRSDSVQVPRRQELF 75
 QY 77 RMAVAADTLQRIQGRVAVSVMGPQQLPDGSLPPVILAEISDPKGVCFYGHLDV 136
 DB 76 RMAVAADTLQRIQGRVAVSVMGPQQLPDGSLPPVILAEISDPKGVCFYGHLDV 135
 QY 137 QPADRGDMLTDPVYLTEVDGKLYGRGATDNKGPVLAIVASAPRALEODLPVNIKEFI 196
 DB 136 QPADRGDMLTDPVYLTEVDGKLYGRGATDNKGPVLAIVASAPRALEODLPVNIKEFI 195
 QY 197 RGMERAGSVALBELVEKEKDRPFSGVDYIVISDNMISORPATYTGRRNSYFWEVKC 256
 DB 196 RGMERAGSVALBELVEKEKDRPFSGVDYIVISDNMISORPATYTGRRNSYFWEVKC 255
 QY 257 RDODFSGTGGILLHEPADIYALLGSLVDSGGHIVPGIYDEVVPLTEESINTYKAHL 316
 DB 256 RDODFSGTGGILLHEPADIYALLGSLVDSGGHIVPGIYDEVVPLTEESINTYKAHL 315
 QY 317 DLEERYNSSRYEKLFDTEKEEILMHLWRYPSLSIHGIEGAFDEPQTKVIPGRVIGKFSI 376
 DB 316 DLEERYNSSRYEKLFDTEKEEILMHLWRYPSLSIHGIEGAFDEPQTKVIPGRVIGKFSI 375
 QY 377 RLVPMMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTGLHPMIANIDTQYLAAKRAIR 436
 DB 376 RLVPMMNVSAVEKQVTRHLEDVFSKRNSSNMVVSMTGLHPMIANIDTQYLAAKRAIR 435
 QY 437 TVFGTEPMIRDSGTIPAKMFOEIVHKSIVLIPGAVDDEHSONEKINMNYIEGKTL 496
 DB 436 TVFGTEPMIRDSGTIPAKMFOEIVHKSIVLIPGAVDDEHSONEKINMNYIEGKTL 495
 QY 497 FAAPFLEMAQLH 508
 DB 496 FAAPFLEMAQLH 507
 RESULT 22
 AEB45360
 ID AEB45360 standard; protein; 507 AA.
 XX
 AC AEB45360;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human wild-type carnosinase 1 protein.
 XX
 KW carnosine metabolism; diabetic nephropathy; neurological disease;
 KW carnosinase 1; CN1; screening; kidney; antidiabetic; neuroprotective;
 KW nephrotropic; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2005064013-A1.
 XX
 PD 14-JUL-2005.
 XX
 PF 23-DEC-2004; 2004WO-EP014696.
 XX
 PR 23-DEC-2003; 2003DE-01060956.
 XX
 PR 12-NOV-2004; 2004EP-00027020.
 XX
 PA (JANS/) JANSSEN B.
 PA (VMOU/) VAN DER WOUDE F.
 XX
 PI Janssen B, Van Der Woude F, Yard B, Peters V, Hohenadel D,
 PI Koepfel H, Baeldje H, De Heer E, Bakker S, Brinkkoetter P;
 DR WPI; 2005-522580/53.
 DR N-PSDB; AEB45359.

XX Use of carnosine metabolism-associated genes, for determining genetic
 PT predisposition/susceptibility to diabetic nephropathy.
 XX
 PS Disclosure, Fig 1; 48pp; English.

CC The invention relates to the use of one or more genes associated with
 CC carnosine metabolism, and/or their variants, and/or their parts, and/or
 CC their 5' and/or 3' flanking regions, for determining diabetic nephropathy
 CC (DN), or an early stage of DN, or a predisposition/susceptibility to DN
 CC Also described are: (1) a method of determining diabetic nephropathy, or
 CC an early stage of DN, or a predisposition/susceptibility to DN, (2) a kit
 CC for determining DN, or an early stage of DN, or a
 CC predisposition/susceptibility to DN, containing one or more reagents for
 CC the determination of the configuration/condition/status of a nucleic acid
 CC associated with carnosine metabolism, at the genomic, transcriptional,
 CC translation and/or post-translational level in a patient sample; and (3)
 CC a method for identifying compounds for the treatment and/or prevention of
 CC DN. The gene associated with carnosine metabolism is the carnosinase 1
 CC (CNI) gene and/or the carnosinase 2 (CN2) gene. The method and kit of the
 CC invention are useful for determining diabetic nephropathy (DN), or an
 CC early stage of DN, or a predisposition/susceptibility to DN. The
 CC screening method is useful for identifying compounds for treating and/or
 CC preventing DN. The method of the invention provides a reliable way of
 CC diagnosing diabetic nephropathy without the need for kidney biopsy. The
 CC disease can be detected at an early stage allowing preventive and/or
 CC therapeutic measures to be started earlier. This sequence represents
 CC human wild-type CNI protein.

XX Sequence 507 AA;

Query Match Best Local Similarity 96.9%; Score 492; DB 9; Length 507;

Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLLGGMFSSPPPALLEKVFQYIDLHODEFVQTLKGVALSDESQVQVPRFRQELP 76
 DB 16 LLLLLLGGMFSSPPPALLEKVFQYIDLHODEFVQTLKGVALSDESQVQVPRFRQELP 75
 QY 77 RMAAVADTLQRLGARAVASVDMGPOQLPDGQSLPIPVYIIAELGSDPTKGTVCYGHLDV 136
 DB 76 RMAAVADTLQRLGARAVASVDMGPOQLPDGQSLPIPVYIIAELGSDPTKGTVCYGHLDV 135
 QY 137 QPADRGGMILDPVYLVTEVNGKLYGRGATNKGVPVLAIVNAVSFRALBEDLPVNIKEFI 196
 DB 136 QPADRGGMILDPVYLVTEVNGKLYGRGATNKGVPVLAIVNAVSFRALBEDLPVNIKEFI 195
 QY 197 EGMEEAGSVALBELVEKEKORFPGVDYIVISDNLMISSKRPATYGTGNSYFMVEVKC 256
 DB 196 EGMEEAGSVALBELVEKEKORFPGVDYIVISDNLMISSKRPATYGTGNSYFMVEVKC 255
 QY 257 RDODFHSHTGGIHEPMADLVALLGSLVDSGGIILVPGIYDEVVPLTSEEINTYKAHL 316
 DB 256 RDODFHSHTGGIHEPMADLVALLGSLVDSGGIILVPGIYDEVVPLTSEEINTYKAHL 315
 QY 317 DLSEYRNSRVEKFLPTKEEILMLMRYPISLHIGEGAPDERGCTTVIPGRVIGKEST 376
 DB 316 DLSEYRNSRVEKFLPTKEEILMLMRYPISLHIGEGAPDERGCTTVIPGRVIGKEST 375
 QY 377 RLVPNNVSAVEKQVTHLEDFESKRNSSNMVSMVMTLGLHPMTANIDTQVYLAAKRAIR 436
 DB 376 RLVPNNVSAVEKQVTHLEDFESKRNSSNMVSMVMTLGLHPMTANIDTQVYLAAKRAIR 435
 QY 437 TVGTGTEDMTRDGGTIIYIAKFOEIVHKSIVLLPLGAVDDGEHSQNEKINRMVYIESTKL 496
 DB 436 TVGTGTEDMTRDGGTIIYIAKFOEIVHKSIVLLPLGAVDDGEHSQNEKINRMVYIESTKL 495
 QY 497 PAAFFLEMAQLH 508
 DB 496 PAAFFLEMAQLH 507

RESULT 23
 AAU28396
 ID AAU28396 standard; protein; 501 AA.
 XX
 AC AAU28396;

XX 03-JAN-2002 (first entry)

XX Amino acid sequence for DPI-45 and DPI-213.

XX Human; depression associated protein isoform; tryptic digest peptide;
 KM DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 KM neuropsychiatric disorder; bipolar mood disorder; neuroleptic; DPI-213;
 KM manic-depressive illness; schizoaffective disorder; DPI-45.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..20 /label= Signal_peptide

FT Protein 21..501 /label= Mature_DPI-45_and_DPI-213

FT Peptide 49..63 /label= Tryptic_peptide

FT Misc-difference 70 /note= "Specifically claimed in claim 4"

FT Peptide /note= "Encoded by ANA"

FT Peptide 306..315 /label= Tryptic_peptide

FT /note= "Specifically claimed in claim 4"

PN WC200162787-A1.

XX 30-ANG-2001.

XX 23-FEB-2001; 2001WO-GB000786.

XX 24-FEB-2000; 2000GB-00004412.

XX 08-DEC-2000; 2000GB-00030050.

XX 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMA, Parekh RB, Rohlf C, Terrett JA, Tyson KI,

XX WPI; 2001-570626/64.

XX N-PSDB; AAS12574.

XX Novel nucleic acid encoding a protein associated with bipolar affective
 PT disorder, which is used for diagnosis, prophylaxis and therapy of
 PT neuropsychiatric disorders, such as bipolar affective disorder.

XX Disclosure; Fig 2B; 153pp; English.

XX The present invention relates to the identification of depression
 CC associated protein isoforms (DPIs), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
 CC affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
 CC increased in BAD subjects. Also described are peptide sequences
 CC identified from DPI-45 and DPI-213 and the nucleic acid sequences they are
 CC encoded by. The sequences of the invention are useful for clinical
 CC screening, diagnosis, prognosis, therapy and prophylaxis of
 CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
 CC BP), manic-depressive illnesses, attention deficit disorders,
 CC schizoaffective disorders, and unipolar affective disorders. The present
 CC sequence represents the amino acid sequence for DPI-45 and DPI-213

XX Sequence 501 AA;

Query Match Best Local Similarity 84.4%; Score 429; DB 4; Length 501;

Matches 429; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

```
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 MAAVAADTLQRLGARVASVDMGPOOLPDGOSLPPIPVIIAELIGSDPTKGTVCFGHLDVQ 137
DB 71 MAAVAADTLQRLGARVASVDMGPOOLPDGOSLPPIPVIIAELIGSDPTKGTVCFGHLDVQ 130
QY 138 PADRGDGLTPPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLBODLPVNIKFIIIE 197
DB 131 PADRGDGLTPPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLBODLPVNIKFIIIE 190
QY 198 GMEBAGSVALEBELVEKEKORFPGSGVDYIVISDNLMISQRKPAITYGTRGNSYFMVEVKCR 257
DB 191 GMEBAGSVALEBELVEKEKORFPGSGVDYIVISDNLMISQRKPAITYGTRGNSYFMVEVKCR 250
QY 258 DDDFSGTGGIILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEBEINTYKAIHLD 317
DB 251 DDDFSGTGGIILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEBEINTYKAIHLD 310
QY 318 LEEYRNSRVEKEFLPDTKEIIMLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
DB 311 LEEYRNSRVEKEFLPDTKEIIMLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370
QY 378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKRVVSWTGLHPWIANIDTQYLAAKRAIRT 437
DB 371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKRVVSWTGLHPWIANIDTQYLAAKRAIRT 430
QY 438 VGTGTPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNYIEGTCLF 497
DB 431 VGTGTPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNYIEGTCLF 490
QY 498 AAFLEMAQ 506
DB 491 AAFLEMAQ 499

RESULT 24
AAU25426
ID AAU25426 standard; protein; 501 AA.
XX
AC AAU25426;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human Schizophrenia-Associated Protein Isoform (SPI) 238/240.
XX
DE Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
KM neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX
OS Homo sapiens.
XX
PN WO200162785-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB000792.
XX
PR 24-FEB-2000; 2000GB-00004415.
XX
PR 28-DEC-2000; 2000US-00750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herach HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
DR WPI: 2001-570624/64.
XX
DR N-PSDB; AAS42478.
XX
PT New schizophrenia associated protein isoforms and encoding nucleic acid
XX molecules, useful for treatment, diagnosis and prognosis of schizophrenia
XX and screening for potential drugs for treatment and new drug targets.
XX
PS Disclosure; Fig 4A; 148pp; English.
XX
XX The sequence represents a schizophrenia-associated protein isoform (SPI).
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CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC in cerebrospinal fluid, serum or plasma and are useful markers of
CC schizophrenia. The sequences can be used for treatment and diagnosis of
CC schizophrenia, screening, prognosis, monitoring the results of therapy,
CC identifying patients most likely to respond to a particular therapy and
CC identification of new targets for drug treatment. SPI DNA is useful as a
CC nucleic acid probe to detect the presence of nucleic acids or SPIs
XX
SQ Sequence 501 AA;
Query Match 84.4%; Score 429; DB 4; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 MAAVAADTLQRLGARVASVDMGPOOLPDGOSLPPIPVIIAELIGSDPTKGTVCFGHLDVQ 137
DB 71 MAAVAADTLQRLGARVASVDMGPOOLPDGOSLPPIPVIIAELIGSDPTKGTVCFGHLDVQ 130
QY 138 PADRGDGLTPPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLBODLPVNIKFIIIE 197
DB 131 PADRGDGLTPPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLBODLPVNIKFIIIE 190
QY 198 GMEBAGSVALEBELVEKEKORFPGSGVDYIVISDNLMISQRKPAITYGTRGNSYFMVEVKCR 257
DB 191 GMEBAGSVALEBELVEKEKORFPGSGVDYIVISDNLMISQRKPAITYGTRGNSYFMVEVKCR 250
QY 258 DDDFSGTGGIILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEBEINTYKAIHLD 317
DB 251 DDDFSGTGGIILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEBEINTYKAIHLD 310
QY 318 LEEYRNSRVEKEFLPDTKEIIMLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
DB 311 LEEYRNSRVEKEFLPDTKEIIMLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370
QY 378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKRVVSWTGLHPWIANIDTQYLAAKRAIRT 437
DB 371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKRVVSWTGLHPWIANIDTQYLAAKRAIRT 430
QY 438 VGTGTPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNYIEGTCLF 497
DB 431 VGTGTPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSQNEKINRWNYIEGTCLF 490
QY 498 AAFLEMAQ 506
DB 491 AAFLEMAQ 499

RESULT 25
AAU15115
ID AAU15115 standard; protein; 501 AA.
XX
AC AAU15115;
XX
DT 24-OCT-2001 (first entry)
XX
DE Schizophrenia-associated isoform SPI-238/240.
XX
DE Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KM neurological disorder; neuropathy.
XX
OS Homo sapiens.
XX
PN WO200163293-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB000783.
XX
PR 24-FEB-2000; 2000GB-00004415.
XX
PR 28-DEC-2000; 2000US-00750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
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PI Herath HMA, Parekh RB, Rohlf C;
 XX WPI; 2001-502868/55.
 DR N-PSDB; AA823811.
 XX
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated features and Schizophrenia Associated Protein
 PT isoforms in samples of cerebrospinal fluid.
 XX
 XX Claim 8; Fig 4A; 160pp; English.

XX The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFA) and SCH
 CC Associated Protein Isoforms (SPI) in samples, e.g. by electrophoresis,
 CC immunosay or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH. The
 CC expression and activity of the SFA, SPIs and related molecules (e.g.
 CC secondary messengers) are studied to diagnose SCH, monitor the progress
 CC of the disorder and the effectiveness of treatment and as targets to
 CC identify and produce potential therapeutic agents for the treatment of
 CC SCH. The paucity of detectable neurally defects distinguishes
 CC neuropsychiatric disorders such as SCH from neurological disorders, where
 CC manifestations of anatomical and biochemical changes have been identified
 CC in many cases. Consequently the identification and characterisation of
 CC cellular and/or molecular causative defects and neuropathies are
 CC necessary for improved treatment of neuropsychiatric disorders. AAU1514-
 CC AAU15762 represent the amino acid sequences of schizophrenia-associated
 CC isoforms used in the method of the invention

XX Sequence 501 AA;

Query Match 84.4%; Score 429; DB 4; Length 501;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MMAVAADTLQRLGARVASVDMGPGQLPDGSLPIPVILAEISDPTKGTVCYGHLDVQ 137
 DB 71 MMAVAADTLQRLGARVASVDMGPGQLPDGSLPIPVILAEISDPTKGTVCYGHLDVQ 130
 QY 138 PAIRGCGMLTDPVYLVFVNDKLYGRGATDNKGPVLAMINVASFRALEQLPVIKRIIE 137
 DB 131 PAIRGCGMLTDPVYLVFVNDKLYGRGATDNKGPVLAMINVASFRALEQLPVIKRIIE 130
 QY 198 GMEASGVALAEELVEKEKDRFSGVDYIVSDNMTISQRPATITGRGNSYFMVEVKCR 257
 DB 191 GMEASGVALAEELVEKEKDRFSGVDYIVSDNMTISQRPATITGRGNSYFMVEVKCR 250
 QY 258 DQFHSGETFGGILHEPMADVLALLGSLVDSGHLVGVYDEVVPLTEESINTYKAHLHD 317
 DB 251 DQFHSGETFGGILHEPMADVLALLGSLVDSGHLVGVYDEVVPLTEESINTYKAHLHD 310
 QY 318 LEEYRNSSRREKFLPTKEEILMLWRYPSLSIHGIGADDEGTIVIGRYIKFSIR 377
 DB 311 LEEYRNSSRREKFLPTKEEILMLWRYPSLSIHGIGADDEGTIVIGRYIKFSIR 370
 QY 378 LVPHMNVSAVEKQVTRHLEDFVSKRNSNKNVSMTGLHPWLANIDPTQYLAAKAIRT 437
 DB 371 LVPHMNVSAVEKQVTRHLEDFVSKRNSNKNVSMTGLHPWLANIDPTQYLAAKAIRT 430
 QY 438 VFGTEPDMIRDSGTIPAKMFOEIVKSVYLLPLGAVDDESHSNKINRMNIEGTCLF 497
 DB 431 VFGTEPDMIRDSGTIPAKMFOEIVKSVYLLPLGAVDDESHSNKINRMNIEGTCLF 490
 QY 498 AAFFLEMAQ 506
 DB 491 AAFFLEMAQ 499

RESULT 26

ADO79056
 ID ADO79056 standard; protein; 501 AA.

XX ADO79056;

DT 26-AUG-2004 (first entry)

XX Schizophrenia-Associated Protein Isoform SPI-238/SPI-240.

XX neuroleptic; Schizophrenia; immunospecific binding;

KM Schizophrenia-Associated Protein Isoform; SPI; schizophrenia screening;

KM Schizophrenia diagnosis; schizophrenia prognosis;

KM Schizophrenia treatment; drug development; cerebrospinal fluid; human;

XX SPI-238; SPI-240.

XX Homo sapiens.

XX US2004110938-A1.

XX 10-JUN-2004.

XX 23-FEB-2001; 2001US-00791377.

XX 24-FEB-2000; 2000GB-00044156.

XX 28-DEC-2000; 2000US-00750395.

XX (PARE/) PAREKH R B.

XX (HERA/) CHANDRASIRI HERATH H M A.

XX (ROHL/) ROHLFF C.

XX (TERR/) TERRETT J A.

XX (TYSON/) TYSON K L.

XX Parekh RB, Chandrasiri Herath HMA, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2004-440403/41.

XX N-PSDB; ADO79056.

XX New isolated nucleic acid molecule, useful for diagnosing Schizophrenia,

PT for monitoring the effectiveness of Schizophrenia treatment or for

PT screening agents for treating Schizophrenia.

XX Disclosure; SEQ ID NO 674; 170pp; English.

XX The invention describes an isolated nucleic acid molecule (I) that

CC hybridises to two short nucleic acid sequences and the 155 amino acid

CC sequence fully defined in the specification. Also described are: a

CC preparation comprising an isolated peptide coded for by the nucleic acid

CC molecule above, or comprising an isolated human protein comprising one or

CC more of the following sequences: Glu-Leu-Asp-Val-Leu-Gly-Arg, and Gly

CC -Ile-Leu-Ile-Gly-Gln-Gln-Asp-Thr-Leu-Gly-Arg; methods for

CC diagnosing Schizophrenia; antibodies capable of immunospecific binding to

CC Schizophrenia-Associated Protein Isoform (SPI); methods of treating

CC Schizophrenia; and methods of screening for agents that modulate a

CC characteristic (e.g., expression or binding activity) of an SPI, an SPI

CC analogue, or an SPI-related polypeptide. The nucleic acid molecule and

CC encoded proteins, as well as the methods and compositions are useful for

CC screening, diagnosing, and prognosing Schizophrenia, for monitoring the

CC effectiveness of Schizophrenia treatment, for identifying patients most

CC likely to respond to a particular therapeutic treatment and for

CC developing drug. They are also useful for screening modulators of

CC Schizophrenia-Associated Protein Isoform useful for treating

CC Schizophrenia. This is the amino acid sequence of schizophrenia-

CC associated protein isoform SPI-238/SPI-240 fusion.

XX Sequence 501 AA;

QY Query Match 84.4%; Score 429; DB 8; Length 501;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MMAVAADTLQRLGARVASVDMGPGQLPDGSLPIPVILAEISDPTKGTVCYGHLDVQ 137

```

Db 71 MAAVAADTLQRLGARVASVDMGPQLPDGSLPIPPVILAEIGSDPTTKGTVCFTGHLVDQ 130
Qy 138 PADRGGMITDPVYLTVVDGKLYGRGATDNKGVPYLAIVANVSAFRLBEDLPVNIKFIIE 197
Db 131 PADRGGMITDPVYLTVVDGKLYGRGATDNKGVPYLAIVANVSAFRLBEDLPVNIKFIIE 190
Qy 198 GMEBAGSVLLEELVEKEDRFPSGVYIYISDNLMTISORPATYTGTRGNSYFMVEVKCR 257
Db 191 GMEBAGSVLLEELVEKEDRFPSGVYIYISDNLMTISORPATYTGTRGNSYFMVEVKCR 250
Qy 258 DDDFHSGTGFIHEPMADLVALLGSLVDSGHIIVPGIYDEVVPLTBEENITYKAIHLD 317
Db 251 DDDFHSGTGFIHEPMADLVALLGSLVDSGHIIVPGIYDEVVPLTBEENITYKAIHLD 310
Qy 318 LBEYRNSRVEKFLPTKKEIILMLMRYSLSIHGEGAPDEGCTTVIPGVYIGFSIR 377
Db 311 LBEYRNSRVEKFLPTKKEIILMLMRYSLSIHGEGAPDEGCTTVIPGVYIGFSIR 370
Qy 378 LVPHMNVSAVEKQVTHLEDVFSKRNSSNKMVSMTLGHPMTANIDPQYLAARKAIRT 437
Db 371 LVPHMNVSAVEKQVTHLEDVFSKRNSSNKMVSMTLGHPMTANIDPQYLAARKAIRT 430
Qy 438 VGTGPEDMIRDSSTPIAQMFOEIVHKSIVYLPLGAVDDGEHSQNEKINRMNYIEGTXLF 497
Db 431 VGTGPEDMIRDSSTPIAQMFOEIVHKSIVYLPLGAVDDGEHSQNEKINRMNYIEGTXLF 490
Qy 498 AAFPLEMAQ 506
Db 491 AAFPLEMAQ 499

RESULT 27
AAB18921
ID AAB18921 standard; protein, 507 AA.
XX
AC AAB18921;
XX
DT 08-FEB-2001 (first entry)
XX
DE A novel polypeptide designated PRO4380.
XX
KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW PRO1889; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW PRO4352; PRO4380; PRO4354; PRO4380; PRO5737; PRO4425; PRO5990; PRO6030;
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW insulinemia; kidney disorder; Bergers disease; nephropathy;
KW Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW Crohns disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..26
FT Modified-site /note= "signal sequence"
FT Modified-site 89..95
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 119..125
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 162..168
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 197..203
FT Modified-site /note= "N-myristoylation site"
FT Misc-difference 230
FT /note= "N-myristoylation site"
FT Modified-site 242..248
FT /note= "Ile encoded by CUG"
FT Modified-site 263..269
FT /note= "N-myristoylation site"
FT Domain /note= "N-myristoylation site"
FT /note= "transmembrane domain"
FT Modified-site 322..326
FT /note= "N-glycosylation site"

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FT Modified-site 351..357
FT /note= "N-myristoylation site"
FT Modified-site 382..386
FT /note= "N-glycosylation site"
FT Modified-site 400..404
FT /note= "cAMP- and cGMP-dependent protein kinase"
FT Modified-site 402..406
FT /note= "N-glycosylation site"
XX
PN WO200056889-A2.
XX
PD 28-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US005601.
XX
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0132919P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 09-DEC-1999; 99US-0170262P.
XX
XX (GENTH ) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WL, Zhang Z;
XX
DR WPI, 2000-628263/60.
DR N-PSDB; AAA96348.
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing tumor
PT in a mammal, for identifying agonists and antagonists of the polypeptide
PT and for therapeutic use.
XX
PS Claim 12, Fig 26; 222pp; English.
XX
CC The present sequence represents a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumor in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells and
CC are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing
XX
SQ Sequence 507 AA;
XX
Qy Query Match 77.0%; Score 391; DB 3; Length 507;
Qy Best Local Similarity 99.8%; Pred. No. 0;
Qy Matches 491; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 17 LLLLLERMFSSPPPALKEVFOYIDHODEFVQTLKEWVAIESDSVQVPRPRQELF 76

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Db      16 LLLLLRGMFSSPPSPALLKRVQYIDLQDEFVQTLKEWVAIESDSVQVPFRROELF 75
Qy      77 RMAVAADTLQRLGARAASVDMGPQLPDGQSLPIPVYLAIGSDPTKGVNCGYGLDV 136
Db      76 RMAVAADTLQRLGARAASVDMGPQLPDGQSLPIPVYLAIGSDPTKGVNCGYGLDV 135
Qy      137 QPADRGDGLTDPVYLTVEVDKLYGRGATDNKGKPVLA MINAVSAFRLBODLPVNIKEII 196
Db      136 QPADRGDGLTDPVYLTVEVDKLYGRGATDNKGKPVLA MINAVSAFRLBODLPVNIKEII 195
Qy      197 EGMEEAGSVALBELVEKRPFGSGVDYIYISDNLMISQKPAITYTGRNGSYFMVEK 256
Db      196 EGMEEAGSVALBELVEKRPFGSGVDYIYISDNLMISQKPAITYTGRNGSYFMVEK 255
Qy      257 RDDDFHSGTGGILHEPMADVLALGSLVDSGHLVPGIYDEVPLTEBEINTYKAHL 316
Db      256 RDDDFHSGTGGILHEPMADVLALGSLVDSGHLVPGIYDEVPLTEBEINTYKAHL 315
Qy      317 DLEBYRNSRVEKPLFDTKKEIIMHLWRYPSLIHGIEGAFDEPGTKVIPGVIGKFSI 376
Db      316 DLEBYRNSRVEKPLFDTKKEIIMHLWRYPSLIHGIEGAFDEPGTKVIPGVIGKFSI 375
Qy      377 RLPVPMNVAASVEKQVTHLEDVSKNSNKMVYSMTLGLHPMIANIDTQYLAAKRAIR 436
Db      376 RLPVPMNVAASVEKQVTHLEDVSKNSNKMVYSMTLGLHPMIANIDTQYLAAKRAIR 435
Qy      437 TVFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGEHSQNEKINRMNYIEGTL 496
Db      436 TVFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGEHSQNEKINRMNYIEGTL 495
Qy      497 FAAFLEMAQLH 508
Db      496 FAAFLEMAQLH 507

```

RESULT 28

AA040149
ID AAM40149 standard; protein; 342 AA.

AC AAM40149,

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3294.

DE Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KM peripheral nervous system; neuropathy; central nervous system; CNS;

KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KM chemokine; thrombolytic; drug screening; arthritis; inflammation;

KM leukemia.

OS Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000MO-US034263.

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
DR WPI, 2001-442253/47.
DR N-PSDB; AAI59305.

PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

PS Example 5; SEQ ID NO 3294; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM38642-AA042213) with nootropic.
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC centralised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 342 AA;

XX Query Match 66.1%; Score 336; DB 4; Length 342;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 AMINAVSAFRLBODLPVNIKEIIEGMEBAGSVALBELVEKRPFGSGVDYIYISDNLM 232
Db 7 AMINAVSAFRLBODLPVNIKEIIEGMEBAGSVALBELVEKRPFGSGVDYIYISDNLM 66

Qy 233 ISGRKPAITVGRNGSYFMVEKRCRDPDPSGTFGGIILHEPMADVLALGSLVDSGHL 292
Db 67 ISGRKPAITVGRNGSYFMVEKRCRDPDPSGTFGGIILHEPMADVLALGSLVDSGHL 126

Qy 293 VPGIYDEVPLTEBEINTYKAHLDEBYRNSRVEKPLFDTKKEIIMHLWRYPSLIHG 352
Db 127 VPGIYDEVPLTEBEINTYKAHLDEBYRNSRVEKPLFDTKKEIIMHLWRYPSLIHG 186

Qy 353 IEGAFDEPGTKTVIPGVIGKFSIRLVPMNVAASVEKQVTHLEDVSKNSNKMVYSMT 412
Db 187 IEGAFDEPGTKTVIPGVIGKFSIRLVPMNVAASVEKQVTHLEDVSKNSNKMVYSMT 246

Qy 413 TGLHPMINIDTQYLAAKRAIRTVFGTEPMIRDSSTPIAKMFOEIVHKSIVLLPLG 472
Db 247 TGLHPMINIDTQYLAAKRAIRTVFGTEPMIRDSSTPIAKMFOEIVHKSIVLLPLG 306

Qy 473 AVDDGEHSQNEKINRMNYIEGTLFAAFLEMAQLH 508
Db 307 AVDDGEHSQNEKINRMNYIEGTLFAAFLEMAQLH 342

RESULT 29

AA041935
ID AAM41935 standard; protein; 358 AA.

AC AAM41935;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6866.

KM Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokine; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.
 XX Homo sapiens.
 OS WO200153312-A1.
 XX
 XX
 XX
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HSE-) HSEQ INC.
 XX
 XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Demanac RT;
 XX
 XX WPI, 2001-442253/47.
 DR N-PSDB; AAI61091.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 PT
 XX
 XX Example 2, SEQ ID NO 6866; 10078pp; English.
 PS
 XX The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AA138642-AA442213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 XX Sequence 358 AA:
 SQ
 Query Match 64.2%; Score 326; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.4e-316;
 Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 273 IDDTYLAAKRAIRVFGTEPDMIRDSSTIPAAKFOEIVHKSVDLPLGAVDDEHSON 332
 QY 483 EKINRMNYIEGTKLPAAFLEMAQLH 508
 DB 333 EKINRMNYIEGTKLPAAFLEMAQLH 358
 RESULT 30
 ADCT7691
 ID ADCT7691 standard; protein; 508 AA.
 XX
 XX AC ADCT7691;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human 55054 protein SEQ ID NO:54.
 XX
 KW pain disorder; pain signalling mechanism; analgesic; antimigraine;
 KW antiinflammatory; gene therapy; inflammatory pain; chronic pain;
 KW neuropathic pain; neuralgia; fibromyalgia; cancer pain; migraine;
 KW headache; pain; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2003073983-A2.
 PN
 XX
 PD 12-SEP-2003.
 XX
 XX 19-FEB-2003; 2003WO-US004816.
 PF
 XX
 XX 28-FEB-2002; 2002US-0360495P.
 PR 04-APR-2002; 2002US-0370121P.
 PR 16-APR-2002; 2002US-0373010P.
 PR 19-APR-2002; 2002US-0373908P.
 PR 03-MAY-2002; 2002US-0377717P.
 PR 13-MAY-2002; 2002US-0379949P.
 PR 21-MAY-2002; 2002US-0382409P.
 PR 03-JUN-2002; 2002US-0385280P.
 PR 06-JUN-2002; 2002US-0386879P.
 PR 10-JUN-2002; 2002US-0394376P.
 PR 08-JUL-2002; 2002US-0394376P.
 PR 21-AUG-2002; 2002US-0404996P.
 PR 19-SEP-2002; 2002US-0412006P.
 PR 09-OCT-2002; 2002US-0417327P.
 PR 10-OCT-2002; 2002US-0417499P.
 PR 15-NOV-2002; 2002US-0426964P.
 PR 10-DEC-2002; 2002US-0432320P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 XX Rosenfeld JB, Silos-Santiago I;
 PI WPI, 2003-712843/67.
 DR N-PSDB; ADCT7690.
 XX
 PT Identifying a compound capable of treating a pain disorder e.g.,
 PT neuropathic pain comprises assaying the ability of the compound to
 PT modulate the nucleic acid expression or polypeptide activity.
 XX
 XX Claim 1; SEQ ID NO 54; 277pp; English.
 PS
 XX The present invention describes a method for identifying a compound (C)
 CC capable of treating a pain disorder comprising assaying the ability of
 CC the compound to modulate 9949, 14230, 760, 62553, 12316, 17719, 41897,
 CC 47174, 33408, 10002, 16209, 314, 636, 27410, 33260, 619, or 13424 nucleic
 CC acid expression or 9949, 14230, 760, 62553, 12316, 17719, 41897, 47174,
 CC 33408, 10002, 16209, 314, 636, 27410, 33260, 619, 15985, polypeptide
 CC activity. Also described: (1) identifying a compound (C) capable of
 CC modulating a pain signalling mechanism; and (2) treating a subject having
 CC a pain disorder characterised by aberrant nucleic acid expression or
 CC polypeptide activity. (C) has analgesic, antimigraine and
 CC antiinflammatory activities, and can be used in gene therapy. The method

CC is useful for identifying a modulator compound capable of treating a pain
CC disorder, e.g. inflammatory pain, chronic pain, neuropathic pain,
CC neuralgia, fibromyalgia, cancer pain, migraine/headache pain or tissue
CC pain comprising administering the modulator to a subject having a pain
CC disorder characterized by aberrant nucleic acid expression or polypeptide
CC activity. The present sequence represents the human 55054 protein from
CC the present invention.
XX

SQ Sequence 508 AA;

Query March 46.3%; Score 235; DB 7; Length 508;

Best Local Similarity 100.0%; Pred. No. 5.3e-225;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	274	MADLVALLGSLVDSSGHLVPGIYDEVVPLTEBEINTYKATHLDLEERYNSSRVEKPLFD	333
Db	274	MADLVALLGSLVDSSGHLVPGIYDEVVPLTEBEINTYKATHLDLEERYNSSRVEKPLFD	333
QY	334	TKBEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR	393
Db	334	TKBEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR	393
QY	394	HLEDFVFSKRNSNKNQVVSMTGLHPWIANIDTOYLAAKRAIRTVFGTEPDMIRDGSTIP	453
Db	394	HLEDFVFSKRNSNKNQVVSMTGLHPWIANIDTOYLAAKRAIRTVFGTEPDMIRDGSTIP	453
QY	454	IAKMFOEIVHKSYYLIPGAVDGDEHSONEKNRMNTEGFKLPAAPFLMAQLH	508
Db	454	IAKMFOEIVHKSYYLIPGAVDGDEHSONEKNRMNTEGFKLPAAPFLMAQLH	508

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Job time : 197 secs

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OM protein - protein search, using SW model

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Title: US-10-849-979-139

Perfect score: 508

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	23.4	148	2	US-09-621-976-3957
2	11	2.2	429	2	US-09-270-767-45937
3	10	2.0	318	2	US-09-581-005-2
4	9	1.8	258	2	US-09-134-000C-4891
5	9	1.8	841	2	US-09-538-092-67
6	8	1.6	16	2	US-09-434-345-4
7	8	1.6	78	2	US-10-178-213-378
8	8	1.6	82	2	US-10-178-213-56
9	8	1.6	100	2	US-09-950-933A-40
10	8	1.6	107	2	US-09-270-767-40343
11	8	1.6	107	2	US-09-270-767-55559
12	8	1.6	115	2	US-09-461-325-160
13	8	1.6	115	2	US-10-012-542-160
14	8	1.6	115	2	US-10-115-123-160
15	8	1.6	115	2	US-09-991-181-95
16	8	1.6	115	2	US-09-990-444-95
17	8	1.6	115	2	US-09-997-333-95
18	8	1.6	115	2	US-09-992-598-95
19	8	1.6	125	2	US-09-621-976-3958
20	8	1.6	136	2	US-09-893-737-150
21	8	1.6	190	2	US-09-893-737-198
22	8	1.6	254	2	US-09-543-681A-7981
23	8	1.6	267	2	US-07-706-872-3
24	8	1.6	277	2	US-09-431-887-14
25	8	1.6	379	2	US-09-107-532A-5519
26	8	1.6	382	2	US-09-902-540-10173
27	8	1.6	402	2	US-09-540-236-2685

28	3	1.6	406	2	US-09-328-352-5309	Sequence 5309, Ap
29	8	1.6	470	2	US-09-543-681A-5952	Sequence 5952, Ap
30	8	1.6	470	2	US-09-502-540-12189	Sequence 12189, Ap
31	8	1.6	493	2	US-09-352-991A-23263	Sequence 23263, A
32	8	1.6	573	2	US-09-252-991A-18744	Sequence 18744, A
33	8	1.6	715	2	US-09-902-540-12939	Sequence 12939, A
34	8	1.6	852	2	US-09-897-427A-6	Sequence 6, Appl1
35	8	1.6	878	2	US-09-826-509-347	Sequence 347, App
36	8	1.6	905	1	US-08-072-574-2	Sequence 2, Appl1
37	8	1.6	906	1	US-08-486-270-2	Sequence 2, Appl1
38	8	1.6	906	2	US-08-367-264-2	Sequence 2, Appl1
39	8	1.6	906	2	US-09-153-757-2	Sequence 2, Appl1
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46	8	1.6	1003	2	US-09-393-795-11	Sequence 11, Appl1
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51	7	1.4	15	2	US-09-500-124-429	Sequence 429, App
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53	7	1.4	25	2	US-09-600-826A-2	Sequence 2, Appl1
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56	7	1.4	37	2	US-09-471-276-825	Sequence 825, App
57	7	1.4	39	2	US-09-270-767-59714	Sequence 59714, A
58	7	1.4	50	2	US-09-205-258-498	Sequence 498, App
59	7	1.4	50	2	US-09-471-276-815	Sequence 815, App
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71	7	1.4	68	2	US-09-248-796A-27784	Sequence 27784, A
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73	7	1.4	75	2	US-08-488-446-407	Sequence 407, App
74	7	1.4	75	2	US-08-467-344A-407	Sequence 407, App
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81	7	1.4	86	2	US-10-027-736A-12	Sequence 12, Appl
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86	7	1.4	95	2	US-09-482-273-234	Sequence 234, App
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93	7	1.4	108	2	US-09-893-737-246	Sequence 246, App
94	7	1.4	111	2	US-09-252-991A-17825	Sequence 17825, A
95	7	1.4	119	2	US-09-583-110-4018	Sequence 4018, Ap
96	7	1.4	114	2	US-09-134-000C-6126	Sequence 6126, Ap
97	7	1.4	117	2	US-09-893-737-208	Sequence 208, App
98	7	1.4	118	2	US-09-248-796A-21734	Sequence 21734, App
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100	7	1.4	120	1	US-08-444-733-181	Sequence 181, App

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101 7 1.4 120 1 US-08-464-134-181 Sequence 181, App
102 7 1.4 120 1 US-08-461-361-181 Sequence 181, App
103 7 1.4 120 1 US-08-485-910-181 Sequence 181, App
104 7 1.4 120 4 PCT-US95-06266-155 Sequence 155, App
105 7 1.4 121 2 US-09-270-767-35492 Sequence 35492, A
106 7 1.4 121 2 US-09-270-767-43149 Sequence 43149, A
107 7 1.4 121 2 US-09-270-767-50709 Sequence 50709, A
108 7 1.4 129 2 US-10-000-489-74 Sequence 74, App
109 7 1.4 130 2 US-09-489-039A-11337 Sequence 11337, A
110 7 1.4 132 2 US-09-107-433-2703 Sequence 2703, App
111 7 1.4 138 2 US-09-902-540-13575 Sequence 13575, A
112 7 1.4 139 1 US-08-466-033-177 Sequence 177, App
113 7 1.4 139 1 US-08-444-733-177 Sequence 177, App
114 7 1.4 139 1 US-08-464-134-177 Sequence 177, App
115 7 1.4 139 1 US-08-461-361-177 Sequence 177, App
116 7 1.4 139 1 US-08-485-910-177 Sequence 177, App
117 7 1.4 139 4 PCT-US95-06266-151 Sequence 151, App
118 7 1.4 150 2 US-09-893-737-230 Sequence 230, App
119 7 1.4 151 2 US-09-621-976-3912 Sequence 3912, App
120 7 1.4 154 2 US-09-248-796A-25445 Sequence 25445, A
121 7 1.4 154 2 US-09-302-540-14147 Sequence 14147, A
122 7 1.4 155 2 US-09-621-976-3888 Sequence 3888, App
123 7 1.4 157 2 US-09-270-767-37259 Sequence 37259, A
124 7 1.4 157 2 US-09-270-767-52476 Sequence 52476, A
125 7 1.4 161 2 US-09-303-518D-280 Sequence 280, App
126 7 1.4 161 2 US-09-303-518D-284 Sequence 284, App
127 7 1.4 168 2 US-09-148-545-280 Sequence 280, App
128 7 1.4 168 2 US-09-621-011-280 Sequence 280, App
129 7 1.4 172 2 US-09-285-601-2 Sequence 2, App
130 7 1.4 172 2 US-09-248-796A-22984 Sequence 22984, A
131 7 1.4 172 2 US-09-949-016-6450 Sequence 6450, App
132 7 1.4 174 2 US-09-383-586-12 Sequence 12, App
133 7 1.4 174 2 US-09-823-038A-12 Sequence 12, App
134 7 1.4 175 2 US-09-248-796A-22939 Sequence 22939, A
135 7 1.4 186 2 US-09-949-016-10375 Sequence 10375, A
136 7 1.4 187 2 US-09-949-016-10543 Sequence 10543, A
137 7 1.4 189 2 US-09-489-039A-8581 Sequence 8581, App
138 7 1.4 190 2 US-09-205-258-423 Sequence 423, App
139 7 1.4 190 2 US-10-004-860-423 Sequence 423, App
140 7 1.4 196 2 US-09-270-767-57435 Sequence 57435, A
141 7 1.4 206 1 US-08-197-793-2 Sequence 2, App
142 7 1.4 206 1 US-08-636-176-2 Sequence 2, App
143 7 1.4 206 4 PCT-US95-01618-2 Sequence 2, App
144 7 1.4 208 2 US-09-615-192A-385 Sequence 385, App
145 7 1.4 210 2 US-09-252-991A-26579 Sequence 26579, A
146 7 1.4 220 2 US-09-252-991A-28942 Sequence 28942, A
147 7 1.4 226 2 US-09-893-737-220 Sequence 220, App
148 7 1.4 227 2 US-09-605-703B-1058 Sequence 1058, App
149 7 1.4 236 2 US-09-902-540-9968 Sequence 9968, App
150 7 1.4 249 2 US-09-489-039A-13124 Sequence 13124, A
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ALIGNMENTS

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RESULT 1
US-09-621-976-3957
; Sequence 3957, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jodard, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3957
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -27...-1
; NAME/KEY: UNSURE
; LOCATION: 93
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; NAME/KEY: UNSURE
; LOCATION: 99
; OTHER INFORMATION: Xaa = Ala, Cys, Asp, Phe, Gly, His, Ile, Leu, Asn, Pro, Arg, Ser, Thr, Val, Tyr
; NAME/KEY: UNSURE
; LOCATION: 102
; OTHER INFORMATION: Xaa = Cys, Ser
; NAME/KEY: UNSURE
; LOCATION: 98
; OTHER INFORMATION: Xaa = Lys, Asn, Arg, Ser, Thr
US-09-621-976-3957
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Query Match 23.4%; Score 119; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 8.4e-106;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MDPKIGMAASLAVLTLLEBGMFSSPPPALLEKVFQYIDHODEFVQTLKEWAI 60
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Qy 61 ESDSVQPVPRFROELFRMMAVAADTLQRLGARVASVDMPGQSLPIPVIIAEL 119
Db 61 ESDSVQPVPRFROELFRMMAVAADTLQRLGARVASVDMPGQSLPIPVIIAEL 119
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RESULT 2
US-09-270-767-45937
; Sequence 45937, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45937
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45937
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Query Match 2.2%; Score 11; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 370 VIGKRSILVP 380
Db 292 VIGKRSILVP 302
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RESULT 3
US-09-581-005-2
; Sequence 2, Application US/09581005
; Patent No. 6825028
; GENERAL INFORMATION:
; APPLICANT: von Bichel-Streibler, Christoph
; APPLICANT: Chakraborty, Trinad
; TITLE OF INVENTION: TGC Method For Inducting Targeted Somatic Transgenesis
; FILE REFERENCE: E 52 P2 MO
; CURRENT APPLICATION NUMBER: US/09/581.005
; CURRENT FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
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ORGANISM: *Listeria monocytogenes* Strain EGDJ/2a
US-09-581-003-2

Query Match 2.0%; Score 10; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKLYGRGATD 166
DB 33 GKLYGRGATD 42

RESULT 4
US-09-134-000C-4891
Sequence 4891, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stramm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4891
LENGTH: 258
TYPE: PRN
ORGANISM: *Enterococcus faecalis*
US-09-134-000C-4891

Query Match 1.8%; Score 9; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 KLYGRGATD 166
DB 128 KLYGRGATD 136

RESULT 5
US-09-538-092-67
Sequence 67, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glaxo, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CnatePatSeqFormater Version 0.9
SEQ ID NO 67
LENGTH: 841
TYPE: PRN
ORGANISM: *Saccharomyces cerevisiae*
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0,...(0)
OTHER INFORMATION: Polypeptide Accession Number YCL054W
US-09-538-092-67

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Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 EVVPLTEEE 307
DB 342 EVVPLTEEE 350

RESULT 6
US-09-434-345-4
Sequence 4, Application US/09434345
Patent No. 6511676
GENERAL INFORMATION:
APPLICANT: Boulikas, Teni
TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING
FILE REFERENCE: TB 2001.00
CURRENT APPLICATION NUMBER: US/09/434,345
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 16
TYPE: PRN
ORGANISM: Duck Hepatitis B Virus
US-09-434-345-4

Query Match 1.6%; Score 8; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 SGTFGGIL 270
DB 2 SGTFGGIL 9

RESULT 7
US-10-178-213-278
Sequence 278, Application US/10178213
Patent No. 6911577
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
TITLE OF INVENTION: Defensein Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 278
LENGTH: 78
TYPE: PRN
ORGANISM: *Triticum aestivum*
US-10-178-213-278

Query Match 1.6%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVTLTLTL 21
DB 10 AVTLTLTL 17

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RESULT 8
US-10-178-213-56
; Sequence 56, Application US/10178213
; Patent No. 6911577
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Hermann, Rafael
; APPLICANT: Mong, James
; TITLE OF INVENTION: Defensein Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-178-213-56
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Best Local Similarity 100.0%; Pred. No. 9.5;
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QY      14 AVLLLLLL 21
Db      12 AVLLLLLL 19

RESULT 9
US-09-950-933A-40
; Sequence 40, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Zea mays
US-09-950-933A-40
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US-09-270-767-40343
; Sequence 40343, Application US/09270767
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40343
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-40343
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Db      80 LAVLLLLL 87
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US-09-270-767-55559
; Sequence 55559, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55559
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-55559
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      80 LAVLLLLL 87
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RESULT 12
US-09-461-325-160
; Sequence 160, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human secreted Proteins
; FILE REFERENCE: P2029p1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
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EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 160
LENGTH: 115
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (96)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-160

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVTLTLL 21
DB 20 AVTLTLL 27

RESULT 13
US-10-012-542-160
Sequence 160, Application US/10012542
Patent No. 6627741
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US/10/012,542
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 160
LENGTH: 115
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (96)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-012-542-160

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVTLTLL 21
DB 20 AVTLTLL 27

RESULT 14
US-10-115-123-160
Sequence 160, Application US/10115123
Patent No. 6774216
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029G30APD2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
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PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 160
LENGTH: 115
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (96)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-160

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVTLTLL 21
DB 20 AVTLTLL 27

RESULT 15
US-09-991-181-95
Sequence 95, Application US/09991181
Patent No. 6913919
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavits, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC53
CURRENT APPLICATION NUMBER: US/09/991,181
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
Db 20 AVLLLLLL 27

RESULT 16
US-09-990-444-95
Sequence 95, Application US/09990444
Patent No. 6930170
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napiet, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/090557
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVLLLL 21
DB 20 AVLLLL 27

RESULT 17
US-09-997-333-95
Sequence 95, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250

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59	PRIOR FILING DATE: 1998-06-10	
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61	PRIOR FILING DATE: 1998-06-11	
62	PRIOR APPLICATION NUMBER: 60/088861	
63	PRIOR FILING DATE: 1998-06-11	
64	PRIOR APPLICATION NUMBER: 60/088876	
65	PRIOR FILING DATE: 1998-06-11	
66	PRIOR APPLICATION NUMBER: 60/089105	
67	PRIOR FILING DATE: 1998-06-12	
68	PRIOR APPLICATION NUMBER: 60/089440	
69	PRIOR FILING DATE: 1998-06-16	

PRIOR APPLICATION NUMBER: 60/089512	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089511	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089533	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089531	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089530	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089529	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089528	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089527	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089526	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089525	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089524	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089523	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089522	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089521	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089520	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089519	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089518	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089517	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089516	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089515	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089513	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512	PRIOR FILING DATE: 1998-06-16

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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match      1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 AVTLLTLL 21
Db      20 AVTLLTLL 27

RESULT 18
US-09-992-598-95
Sequence 95, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyer, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/083598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/083599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/083600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/083653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/083801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/083907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01

PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092162
PRIOR FILING DATE: 1998-07-09

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLL 21
Db 20 AVLLLLL 27

RESULT 19
US-09-621-976-3958
Sequence 3958, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3958
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -92..-1
US-09-621-976-3958

Query Match 1.6%; Score 8; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVALLL 19
Db 84 LLAVALLL 91

RESULT 20
US-09-893-737-150
Sequence 150, Application US/09893737
Patent No. 6822082
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 150
LENGTH: 136
TYPE: PRT
ORGANISM: Homo sapiens

US-09-893-737-150

Query Match 1.6%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LVLLLLL 22
DB 3 VLLLLLL 10

RESULT 21

US-09-893-737-198
Sequence 198, Application US/09893737
Patent No. 6822082
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 198
LENGTH: 190
TYPE: PRT
ORGANISM: Homo sapiens
US-09-893-737-198

US-09-893-737-198

Query Match 1.6%; Score 8; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVLLLLL 21
DB 20 AVLLLLL 27

RESULT 22

US-09-543-681A-7981
Sequence 7981, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEINS MIRABILIS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7981
LENGTH: 254
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7981

Query Match 1.6%; Score 8; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 PLTEERIN 309
DB 241 PLTEERIN 248

RESULT 23
US-07-706-872-3
Sequence 3, Application US/07706872

Patent No. 5237056
GENERAL INFORMATION:
APPLICANT: Fischbach, Gerald D.
TITLE OF INVENTION: Identification of a Protein Which
TITLE OF INVENTION: Promotes the Synthesis of Acetylcholine Receptors and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/706,872
FILING DATE: 19910529
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: H091-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-706-872-3

Query Match 1.6%; Score 8; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LAVLLLL 20
DB 253 LAVLLLL 260

RESULT 24

US-09-431-887-34
Sequence 34, Application US/09431887
Patent No. 6534036
GENERAL INFORMATION:
APPLICANT: D-Gen Limited
TITLE OF INVENTION: BIOLOGICAL MATERIALS AND METHODS USEFUL IN THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PRION DISEASE
FILE REFERENCE: ICOT/P21952
CURRENT APPLICATION NUMBER: US/09/431,887
CURRENT FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: GB 9824091.4
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 277
TYPE: PRT
ORGANISM: Gallus gallus
US-09-431-887-34

Query Match 1.6%; Score 8; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LAVLLLL 20

Db 263 LAVLLLLL 270

RESULT 25
US-09-107-532A-5519
; Sequence 5519, Application US/09107532A
; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: LYNN A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5519:

SEQUENCE CHARACTERISTICS:

LENGTH: 379 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...379

SEQUENCE DESCRIPTION: SEQ ID NO: 5519:

Query Match 1.6%; Score 8; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 LYRGATD 166
Db 97 LYRGATD 104

RESULT 26
US-09-902-540-10173
; Sequence 10173, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10173
; LENGTH: 382
; TYPE: PRF
; ORGANISM: Myxococcus xanthus

US-09-902-540-10173

Query Match 1.6%; Score 8; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVALLLL 19
Db 35 LVALLLL 42

RESULT 27
US-09-540-236-2685
; Sequence 2685, Application US/09540236
; Patent No. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI

FILE REFERENCE: 2709,2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2685

LENGTH: 402

TYPE: PRF

ORGANISM: M. catarrhalis

US-09-540-236-2685

Query Match 1.6%; Score 8; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKLYGRGA 164
Db 112 GKLYGRGA 119

RESULT 28
US-09-328-352-5309
; Sequence 5309, Application US/09328352
; Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 5309

LENGTH: 406

TYPE: PRF

ORGANISM: Acinetobacter baumannii

US-09-328-352-5309

Query Match 1.6%; Score 8; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 DGKLYGRG 163
Db 111 DGKLYGRG 118

Db 120 DGLYGRG 127

RESULT 29
US-09-543-681A-5952
; Sequence 5952, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5952
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5952

Query Match 1.6%; Score 8; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 VLLILLLE 22
|||||||
Db 38 VLLILLLE 45

RESULT 30
US-09-902-540-12189
; Sequence 12189, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12189
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12189

Query Match 1.6%; Score 8; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LGRMAASL 12
|||||||
Db 395 LGRMAASL 402

Search completed: March 30, 2006, 09:13:24
Job time : 48 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2006, 09:12:47 ; Search time 168 Seconds
(without alignment)
1263.436 Million cell updates/sec

Title: US-10-849-979-139

Perfect score: 508

Sequence: 1 MDPKLGMAASLAVLLLL.....NYIEGTLFAFLEMAQLH 508

Scoring table: OLIGO

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Word size : 6

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Post-processing: Listing first 150 summaries

Database :

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	100.0	508	US-09-731-872-242	Sequence 242, App
2	508	100.0	508	US-09-948-783-139	Sequence 139, App
3	508	100.0	508	US-09-876-997-242	Sequence 242, App
4	508	100.0	508	US-10-643-836-242	Sequence 242, App
5	508	100.0	508	US-10-472-533-371	Sequence 371, App
6	508	100.0	509	US-09-892-877-137	Sequence 137, App
7	492	96.9	507	US-09-963-280-2	Sequence 2, App1
8	492	96.9	507	US-09-931-836-57	Sequence 57, App1
9	492	96.9	507	US-10-036-342-57	Sequence 57, App1
10	492	96.9	507	US-10-036-041-57	Sequence 57, App1
11	492	96.9	507	US-10-035-855-57	Sequence 57, App1
12	492	96.9	507	US-10-036-214-57	Sequence 57, App1
13	492	96.9	507	US-10-035-719-57	Sequence 57, App1
14	492	96.9	507	US-10-036-160-57	Sequence 57, App1
15	492	96.9	507	US-10-035-958-57	Sequence 57, App1
16	492	96.9	507	US-10-036-150-57	Sequence 57, App1
17	492	96.9	507	US-10-036-063-57	Sequence 57, App1
18	492	96.9	507	US-10-035-977-57	Sequence 57, App1
19	492	96.9	507	US-10-275-107-68	Sequence 68, App1
20	492	96.9	507	US-10-884-091-57	Sequence 57, App1
21	429	84.4	501	US-09-791-378-674	Sequence 674, App
22	429	84.4	501	US-09-791-393-2	Sequence 2, App1
23	429	84.4	501	US-09-791-389-2	Sequence 2, App1
24	429	84.4	501	US-09-791-377-674	Sequence 674, App
25	235	46.3	508	US-10-369-022-54	Sequence 54, App
26	126	24.8	133	US-10-296-115-1427	Sequence 1427, App
27	100	19.7	316	US-10-264-237-2057	Sequence 2057, App

28	10.6	100	5	US-10-450-763-32013	Sequence 32013, A
29	7.3	157	5	US-10-450-763-32012	Sequence 32012, A
30	3.0	15	3	US-09-791-378-199	Sequence 199, App
31	3.0	15	3	US-09-791-378-657	Sequence 657, App
32	3.0	15	3	US-09-791-393-297	Sequence 297, App
33	3.0	15	3	US-09-791-389-297	Sequence 297, App
34	3.0	15	3	US-09-791-377-199	Sequence 199, App
35	3.0	15	3	US-09-791-377-657	Sequence 657, App
36	2.8	14	3	US-09-791-378-201	Sequence 201, App
37	2.8	14	3	US-09-791-378-665	Sequence 665, App
38	2.8	14	3	US-09-791-377-201	Sequence 201, App
39	2.8	14	3	US-09-791-377-665	Sequence 665, App
40	2.2	11	3	US-09-791-378-202	Sequence 202, App
41	2.2	11	3	US-09-791-377-202	Sequence 202, App
42	2.2	11	3	US-09-791-378-206	Sequence 206, App
43	2.2	11	3	US-09-791-377-200	Sequence 200, App
44	2.2	11	3	US-09-791-377-206	Sequence 206, App
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49	2.0	10	3	US-09-791-378-667	Sequence 667, App
50	2.0	10	3	US-09-791-393-308	Sequence 308, App
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97	1.8	194	4	US-10-227-882-32	Sequence 32, App1
98	1.8	194	4	US-10-230-436-32	Sequence 32, App1
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138 9 1.8 194 4 US-10-219-527-32 Sequence 32, Appl
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ALIGNMENTS

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RESULT 1
US-09-731-872-242
/ Sequence 242, Application US/09731872
/ Patent No. US20020102604A1
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, Jean Baptiste
/ APPLICANT: Bougueterec, Lydie
/ TITLE OF INVENTION: FULL-LENGTH HUMAN CDNA8 ENCODING POTENTIALLY SECRETED PROTEINS
/ FILE REFERENCE: 78 US3 REG
/ CURRENT APPLICATION NUMBER: US/09/731, 872
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/169, 629
/ PRIOR FILING DATE: 1999-12-08
/ PRIOR APPLICATION NUMBER: US 60/187, 470
/ PRIOR FILING DATE: 2000-03-06
/ NUMBER OF SEQ ID NOS: 482
/ SOFTWARE: Patent.pm
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/ SEQ ID NO 242
/ LENGTH: 508
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE: SIGNAL
/ NAME/KEY: SIGNAL
/ LOCATION: -27...-1
US-09-731-872-242
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Query Match 100.0%; Score 508; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 508; Conservative 0;
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DB 61 ESDSVQVPRPRROELFRMAVAADTLQRLGARVASVDMGPPOOLPFGSULPIPPVLAELG 120
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DB 121 SDPTKGTVCYFGHLDVOPADRGDGLTPVYLTEVDGKLYGRGATDNKGPTVLAIVASA 180
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DB 181 FRALRQDLPVNIKFIIIEGMEASGVALBELVEKEKORFFSGVDYIVISDNIMISQRKPAI 240
QY 241 TYGTGNSYFVWEVCKRQDPSGTFGGILHBPADIVALLGSLVDSGHLVPGIYBEV 300
DB 241 TYGTGNSYFVWEVCKRQDPSGTFGGILHBPADIVALLGSLVDSGHLVPGIYBEV 300
QY 301 VPLTEELINTYKAHLHDEEYRNSGRVEKFLPDTKEBILMLMRPSSIIGIEGAPDBP 360
DB 301 VPLTEELINTYKAHLHDEEYRNSGRVEKFLPDTKEBILMLMRPSSIIGIEGAPDBP 360
QY 361 GKTIVIPGRVIGKFSIRLVPMNVSAVEKQYTRHLEDVFSKRNSNKNVSWTGLAHPMI 420
DB 361 GKTIVIPGRVIGKFSIRLVPMNVSAVEKQYTRHLEDVFSKRNSNKNVSWTGLAHPMI 420
QY 421 ANIDTQYLAARARTYGTPEPMIRDSITPIAKMQEIVHKSVALPLGAVDDGSHS 480
DB 421 ANIDTQYLAARARTYGTPEPMIRDSITPIAKMQEIVHKSVALPLGAVDDGSHS 480
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DB 481 QNEKINRMNYIEGTLFAAFLEMAQLH 508
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RESULT 2
US-09-948-783-139
/ Sequence 139, Application US/09948783
/ Publication No. US20030100051A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et. al.
/ TITLE OF INVENTION: 97 Human secreted proteins
/ FILE REFERENCE: P2028P2
/ CURRENT APPLICATION NUMBER: US/09/948, 783
/ CURRENT FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/231, 846
/ PRIOR FILING DATE: 2000-09-11
/ PRIOR APPLICATION NUMBER: 09/892, 877
/ PRIOR FILING DATE: 2001-06-28
/ PRIOR APPLICATION NUMBER: 09/437, 658
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: PCT/US99/09847
/ PRIOR FILING DATE: 1999-05-06
/ PRIOR APPLICATION NUMBER: 60/085, 093
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: 60/085, 094
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: 60/085, 105
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; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,928
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,920
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 139
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-948-783-139

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Query Match 100.0%; Score 508; DB 3; Length 508;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDPLGRMAASLAVLALLLERGMFSSPPPALLEKRYQYIDLDHDEFVQTLKEWVAI 60
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DB 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEIG 120
QY 121 SDPTKTGTCFYGHLDVQPADRGDGLTDPYVLTENVGKLYGKATDNKGPVLAMINAVSA 180
DB 121 SDPTKTGTCFYGHLDVQPADRGDGLTDPYVLTENVGKLYGKATDNKGPVLAMINAVSA 180
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DB 181 FRALBODLPVNIKFIIEGMEBAGSVALLEVEKEKDRFSGVDYIYISNLMISQKRPAT 240
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DB 241 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLSLVDSGHIILVPGIYDEV 300
QY 301 VPLTEEEINTYKAIHLDLEBYRNSRVEKFLDTKEEILMHLWRYPSSLIHGIEGAFDEP 360
DB 301 VPLTEEEINTYKAIHLDLEBYRNSRVEKFLDTKEEILMHLWRYPSSLIHGIEGAFDEP 360
QY 361 GIKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDEVFSKNSNKMVSMTLGLHPWI 420
DB 361 GIKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDEVFSKNSNKMVSMTLGLHPWI 420
QY 421 ANIDDTQYLAARAIKRTVFGTEPDMIRDSSTIPAKMFOEIVHKSIVLILPLGAVDGEHS 480
DB 421 ANIDDTQYLAARAIKRTVFGTEPDMIRDSSTIPAKMFOEIVHKSIVLILPLGAVDGEHS 480
QY 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508
DB 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508

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RESULT 3
US-09-876-997-242
; Sequence 242, Application US/09876997

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; Publication No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouguerelet, Lydie
; APPLICANT: Ubert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNA5 ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.USA.CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 242
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -27...-1
US-09-876-997-242

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Query Match 100.0%; Score 508; DB 3; Length 508;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDPLGRMAASLAVLALLLERGMFSSPPPALLEKRYQYIDLDHDEFVQTLKEWVAI 60
QY 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEIG 120
DB 61 ESDSVQVPRFRQELFRMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPPVILAEIG 120
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DB 181 FRALBODLPVNIKFIIEGMEBAGSVALLEVEKEKDRFSGVDYIYISNLMISQKRPAT 240
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DB 241 TYGTRGNSYFMVEVKCRDQDFHSGTGGILHEPMADLVALLSLVDSGHIILVPGIYDEV 300
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DB 301 VPLTEEEINTYKAIHLDLEBYRNSRVEKFLDTKEEILMHLWRYPSSLIHGIEGAFDEP 360
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DB 481 ONEKINRMNYIEGTKLFAAFPLEMAQLH 508

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RESULT 4
US-10-643-836-242
; Sequence 242, Application US/10643836
; Publication No. US20050096458A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste

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/ APPLICANT: Bougueleret, Lydie
/ APPLICANT: Jobert, Severin
/ TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
/ FILE REFERENCE: 78.US3.REG
/ CURRENT APPLICATION NUMBER: US/10/643,836
/ CURRENT FILING DATE: 2003-08-19
/ PRIOR APPLICATION NUMBER: US/09/731,872
/ PRIOR FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/169,629
/ PRIOR FILING DATE: 1999-12-08
/ PRIOR APPLICATION NUMBER: US 60/187,470
/ PRIOR FILING DATE: 2000-03-06
/ NUMBER OF SEQ ID NOS: 482
/ SOFTWARE: Patent.pm
/ SEQ ID NO 242
/ LENGTH: 508
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIGNAL
/ LOCATION: -27..-1
/ US-10-643-836-242
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Query Match      100.0%; Score 508; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDPKLGMAASLAVLTLILLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
DB 1 MDPKLGMAASLAVLTLILLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
QY 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
DB 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
QY 121 SDPTKGTVCFGHLDVQPADRGDGLTDPVYLTEVDGKLYRGATDNKGPVLAMINAVSA 180
DB 121 SDPTKGTVCFGHLDVQPADRGDGLTDPVYLTEVDGKLYRGATDNKGPVLAMINAVSA 180
QY 121 TYGTRGNSYFMVEYKCRDQDPSHGTGGILHEPMADLVALGSLVDSGHIILVPGIYDEV 300
DB 121 TYGTRGNSYFMVEYKCRDQDPSHGTGGILHEPMADLVALGSLVDSGHIILVPGIYDEV 300
QY 181 FRALBODLPVNIKFIIEGMEAGSVALLEIVEKEKDRFSGVDYIVISDNLMISQKPAI 240
DB 181 FRALBODLPVNIKFIIEGMEAGSVALLEIVEKEKDRFSGVDYIVISDNLMISQKPAI 240
QY 241 TYGTRGNSYFMVEYKCRDQDPSHGTGGILHEPMADLVALGSLVDSGHIILVPGIYDEV 300
DB 241 TYGTRGNSYFMVEYKCRDQDPSHGTGGILHEPMADLVALGSLVDSGHIILVPGIYDEV 300
QY 301 VPLTEEBEINTYKAHLDEEYRNSRVEKFLPTKEELMLHMRYPSSLIHGIEGAFDEP 360
DB 301 VPLTEEBEINTYKAHLDEEYRNSRVEKFLPTKEELMLHMRYPSSLIHGIEGAFDEP 360
QY 361 GTRKTVIPGRVIGKFSIRLVPHMNVSAVEKQYTRHLEDFVSRRNSNKNVSMITGLHPMI 420
DB 361 GTRKTVIPGRVIGKFSIRLVPHMNVSAVEKQYTRHLEDFVSRRNSNKNVSMITGLHPMI 420
QY 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTITIAKMFQEIYHKSIVLIPGAVDGSHS 480
DB 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTITIAKMFQEIYHKSIVLIPGAVDGSHS 480
QY 481 ONEKINRMNVIETGKLFAPAFLEMAQLH 508
DB 481 ONEKINRMNVIETGKLFAPAFLEMAQLH 508
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RESULT 5
US-10-472-533-371

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/ Sequence 371, Application US/10/472533
/ Publication No. US20050197285A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ TITLE OF INVENTION: Human Secreted Proteins
/ FILE REFERENCE: PS966PCT
/ CURRENT APPLICATION NUMBER: US/10/472,533
```

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/ CURRENT FILING DATE: 2003-09-20
/ PRIOR APPLICATION NUMBER: US 60/331,287
/ PRIOR FILING DATE: 2001-11-13
/ PRIOR APPLICATION NUMBER: US 60/306,171
/ PRIOR FILING DATE: 2001-07-19
/ PRIOR APPLICATION NUMBER: US 60/277,340
/ PRIOR FILING DATE: 2001-03-21
/ NUMBER OF SEQ ID NOS: 650
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 371
/ LENGTH: 508
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-472-533-371
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Query Match      100.0%; Score 508; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDPKLGMAASLAVLTLILLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
DB 1 MDPKLGMAASLAVLTLILLERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEWVAI 60
QY 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
DB 61 ESDSVQVPRFRROELFRMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPVILAEIG 120
QY 121 SDPTKGTVCFGHLDVQPADRGDGLTDPVYLTEVDGKLYRGATDNKGPVLAMINAVSA 180
DB 121 SDPTKGTVCFGHLDVQPADRGDGLTDPVYLTEVDGKLYRGATDNKGPVLAMINAVSA 180
QY 181 FRALBODLPVNIKFIIEGMEAGSVALLEIVEKEKDRFSGVDYIVISDNLMISQKPAI 240
DB 181 FRALBODLPVNIKFIIEGMEAGSVALLEIVEKEKDRFSGVDYIVISDNLMISQKPAI 240
QY 241 TYGTRGNSYFMVEYKCRDQDPSHGTGGILHEPMADLVALGSLVDSGHIILVPGIYDEV 300
DB 241 TYGTRGNSYFMVEYKCRDQDPSHGTGGILHEPMADLVALGSLVDSGHIILVPGIYDEV 300
QY 301 VPLTEEBEINTYKAHLDEEYRNSRVEKFLPTKEELMLHMRYPSSLIHGIEGAFDEP 360
DB 301 VPLTEEBEINTYKAHLDEEYRNSRVEKFLPTKEELMLHMRYPSSLIHGIEGAFDEP 360
QY 361 GTRKTVIPGRVIGKFSIRLVPHMNVSAVEKQYTRHLEDFVSRRNSNKNVSMITGLHPMI 420
DB 361 GTRKTVIPGRVIGKFSIRLVPHMNVSAVEKQYTRHLEDFVSRRNSNKNVSMITGLHPMI 420
QY 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTITIAKMFQEIYHKSIVLIPGAVDGSHS 480
DB 421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTITIAKMFQEIYHKSIVLIPGAVDGSHS 480
QY 481 ONEKINRMNVIETGKLFAPAFLEMAQLH 508
DB 481 ONEKINRMNVIETGKLFAPAFLEMAQLH 508
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RESULT 6
US-09-892-877-137

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/ Sequence 137, Application US/09892877
/ Publication No. US20030077809A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et. al.
/ TITLE OF INVENTION: 97 Human secreted proteins
/ FILE REFERENCE: P2028P1
/ CURRENT APPLICATION NUMBER: US/09/892,877
/ CURRENT FILING DATE: 2001-06-28
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
/ NUMBER OF SEQ ID NOS: 461
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 137
/ LENGTH: 509
/ TYPE: PRT
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ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: SITE
 LOCATION: (509)
 OTHER INFORMATION: Xaa equals stop translation
 US-09-892-877-137

Query Match 100.0%; Score 508; DB 3; Length 509;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPVLGMAASLAVLLLLLEERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEMVAI 60
 DB 1 MDPVLGMAASLAVLLLLLEERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEMVAI 60
 QY 61 ESDSVQVPRFRQRLFRMMVAADTLQRLGARVASVDMGPQQLPDGQSLPFPVILAEIG 120
 DB 61 ESDSVQVPRFRQRLFRMMVAADTLQRLGARVASVDMGPQQLPDGQSLPFPVILAEIG 120
 QY 121 SDPTKGTVCYFGHLDVQPADRGDMLTDPYVLTEVDGKLYGRGATDNKGPVLAMINAVSA 180
 DB 121 SDPTKGTVCYFGHLDVQPADRGDMLTDPYVLTEVDGKLYGRGATDNKGPVLAMINAVSA 180
 QY 181 FRALEQDLPVNIKEIIEGMEBAGSVALBELVEKEKDRFFSGVDYIYISDNLMISQKPAI 240
 DB 181 FRALEQDLPVNIKEIIEGMEBAGSVALBELVEKEKDRFFSGVDYIYISDNLMISQKPAI 240
 QY 241 TYGGRGNSYFMVNEKCRDOPHSGTGGILHEPMADVLALGSLVDSGSHLVPGIYDEV 300
 DB 241 TYGGRGNSYFMVNEKCRDOPHSGTGGILHEPMADVLALGSLVDSGSHLVPGIYDEV 300
 QY 301 VPLTEEBINTYKAHLLEERYNSRYEKLFDTKEEILMLMRYPSSLIHGIEGAFDEP 360
 DB 301 VPLTEEBINTYKAHLLEERYNSRYEKLFDTKEEILMLMRYPSSLIHGIEGAFDEP 360
 QY 361 GTKTVIFGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKNSNKNVSMTLGLHPWI 420
 DB 361 GTKTVIFGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDFVSKNSNKNVSMTLGLHPWI 420
 QY 421 ANIDDOYLAAKRAIRVFTGERPMIDGSTIPIAKMFOEIVKSVLILPLGAVDGEHS 480
 DB 421 ANIDDOYLAAKRAIRVFTGERPMIDGSTIPIAKMFOEIVKSVLILPLGAVDGEHS 480
 QY 481 QNEKINRMNYIEGFKLPAFFLEMAQLH 508
 DB 481 QNEKINRMNYIEGFKLPAFFLEMAQLH 508

RESULT 7

US-09-963-290-2
 Sequence 2, Application US/09963290
 Patent No. US20020137713A1
 GENERAL INFORMATION:
 APPLICANT: Kapeller-Libermann, Rosana
 TITLE OF INVENTION: 55054, A No. US20020137713A1 Human Metalloprotease and Uses Thereof
 FILE REFERENCE: 10147-47V1
 CURRENT APPLICATION NUMBER: US/09/963,290
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US 60/235,055
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 507
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-963-290-2

Query Match 96.9%; Score 492; DB 3; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 LLLLEERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEMVAIESDSVQVPRFRQELP 76

DB 16 LLLLEERGMFSSPPPALLEKVFQYIDLHODEFVQTLKEMVAIESDSVQVPRFRQELP 75
 QY 77 RMAVAADTLQRLGARVASVDMGPQQLPDGQSLPFPVILAEIGSDPTKGTVCYFGHLDV 136
 DB 76 RMAVAADTLQRLGARVASVDMGPQQLPDGQSLPFPVILAEIGSDPTKGTVCYFGHLDV 135
 QY 137 QPADRGDMLTDPYVLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPVNIKEFI 196
 DB 136 QPADRGDMLTDPYVLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPVNIKEFI 195
 QY 197 EGMEEBAGSVALBELVEKEKDRFFSGVDYIYISDNLMISQKPAITYGGRNSYFMVNEVC 256
 DB 196 EGMEEBAGSVALBELVEKEKDRFFSGVDYIYISDNLMISQKPAITYGGRNSYFMVNEVC 255
 QY 257 RQDDFHSSTFGGILHEPMADVLALGSLVDSGSHLVPGIYDEVVPLTEEBINTYKAHL 316
 DB 256 RQDDFHSSTFGGILHEPMADVLALGSLVDSGSHLVPGIYDEVVPLTEEBINTYKAHL 315
 QY 317 DLEERYNSRYEKLFDTKEEILMLMRYPSSLIHGIEGAFDEPRTKTVIPGRVIGKFSI 376
 DB 316 DLEERYNSRYEKLFDTKEEILMLMRYPSSLIHGIEGAFDEPRTKTVIPGRVIGKFSI 375
 QY 377 RLVPHMNVSAVEKQVTRHLEDFVSKNSNKNVSMTLGLHPMIANIDDOYLAAKRAIR 436
 DB 376 RLVPHMNVSAVEKQVTRHLEDFVSKNSNKNVSMTLGLHPMIANIDDOYLAAKRAIR 435
 QY 437 TYGTEPDMIRDGSTIPIAKMFOEIVKSVLILPLGAVDGEHSQNEKINRMNYIEGFKL 496
 DB 436 TYGTEPDMIRDGSTIPIAKMFOEIVKSVLILPLGAVDGEHSQNEKINRMNYIEGFKL 495
 QY 497 FFAFFLEMAQLH 508
 DB 496 FFAFFLEMAQLH 507

RESULT 8

US-09-931-836-57
 Sequence 57, Application US/09931836
 Publication No. US20030027249A1
 GENERAL INFORMATION:
 APPLICANT: Deenoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3030R1C1
 CURRENT APPLICATION NUMBER: US/09/931,836
 PRIOR FILING DATE: 2001-08-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/112514
 PRIOR FILING DATE: 1998-12-15
 PRIOR APPLICATION NUMBER: 60/113300
 PRIOR FILING DATE: 1998-12-22
 PRIOR APPLICATION NUMBER: 60/113430
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 60/113605
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 60/113621
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 60/114140
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 60/115552
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/116843

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/ PRIOR FILING DATE: 1999-01-22
/ PRIOR APPLICATION NUMBER: 60/125774
/ PRIOR FILING DATE: 1999-03-23
/ PRIOR APPLICATION NUMBER: 60/125778
/ PRIOR FILING DATE: 1999-03-23
/ PRIOR APPLICATION NUMBER: 60/125826
/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: 60/127035
/ PRIOR FILING DATE: 1999-03-31
/ PRIOR APPLICATION NUMBER: 60/127706
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: 60/129122
/ PRIOR FILING DATE: 1999-04-13
/ PRIOR APPLICATION NUMBER: 60/130359
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: 60/131270
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/131272
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/131291
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/132371
/ PRIOR FILING DATE: 1999-05-04
/ PRIOR APPLICATION NUMBER: 60/132379
/ PRIOR FILING DATE: 1999-05-04
/ PRIOR APPLICATION NUMBER: 60/132383
/ PRIOR FILING DATE: 1999-05-04
/ PRIOR APPLICATION NUMBER: 60/135750
/ PRIOR FILING DATE: 1999-05-25
/ PRIOR APPLICATION NUMBER: 60/138166
/ PRIOR FILING DATE: 1999-06-08
/ PRIOR APPLICATION NUMBER: 60/144791
/ PRIOR FILING DATE: 1999-07-20
/ PRIOR APPLICATION NUMBER: 60/146970
/ PRIOR FILING DATE: 1999-08-03
/ PRIOR APPLICATION NUMBER: 60/162506
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: 09/311832
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/380142
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 09/644848
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 09/747259
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 09/816744
/ PRIOR FILING DATE: 2001-03-22
/ PRIOR APPLICATION NUMBER: 09/854208
/ PRIOR FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 09/854280
/ PRIOR FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 09/874503
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/869599
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: 09/908, 827
/ PRIOR FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: PCT/US99/10733
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: PCT/US99/28551
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30720
/ PRIOR FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: PCT/US00/05601
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: 2000-03-02
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: PCT/US00/15264
/ PRIOR FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US00/34956
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: 2001-06-28
/ PRIOR APPLICATION NUMBER: PCT/US01/17800
/ PRIOR FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: PCT/US01/19692
/ PRIOR FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21066
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 80
/ SEQ ID NO 57
/ LENGTH: 507
/ TYPE: prt
/ ORGANISM: Homo Sapien
/ US-09-931-836-57

Query Match      96.9%; Score 492; DB 3; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17      LLLLLLRRGMFSSPPSPALLKRVFOYIDLHODEFVQTLKEWVAIESDSVQVPRRROELF 76
DB      16      LLLLLLRRGMFSSPPSPALLKRVFOYIDLHODEFVQTLKEWVAIESDSVQVPRRROELF 75
QY      77      RMMVAADTLQRLGARVSVVMGPOQLPDGSLPIPPVITLAEIGSDPFGKVCFFGHLDV 136
DB      76      RMMVAADTLQRLGARVSVVMGPOQLPDGSLPIPPVITLAEIGSDPFGKVCFFGHLDV 135
QY      137      QPADRGDMLTDPYVLTEVDGLYGRGATDNKGPVLAWINAVSAFRALEODLPVNIKEFI 196
DB      136      QPADRGDMLTDPYVLTEVDGLYGRGATDNKGPVLAWINAVSAFRALEODLPVNIKEFI 195
QY      197      EGMEBAGSVALEBEVEKEKDRFFSGVDYIVISDNLMISORRPAITYTGRGNSYFWEVVKC 256
DB      196      EGMEBAGSVALEBEVEKEKDRFFSGVDYIVISDNLMISORRPAITYTGRGNSYFWEVVKC 255
QY      257      RDQDFHSTFGGILHEPMAADLVALLGSLVDSGGHILVNGIYDEVVPLTEESINTYKAHL 316
DB      256      RDQDFHSTFGGILHEPMAADLVALLGSLVDSGGHILVNGIYDEVVPLTEESINTYKAHL 315
QY      317      DLEERYNSRYVEKFLFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIFGRVIGKFSI 376
DB      316      DLEERYNSRYVEKFLFTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIFGRVIGKFSI 375
QY      377      RLVPHMNVSAVEKQVTRHLEDFVFSKRNSNMVVSMTGLHPWIANIDTQYLAAKRAIR 436
DB      376      RLVPHMNVSAVEKQVTRHLEDFVFSKRNSNMVVSMTGLHPWIANIDTQYLAAKRAIR 435
QY      437      TVFGTEPMDIGSTIPLAKKFORIVHKSIVLILPGANDDEHONKINMNYIEGKRL 496
DB      436      TVFGTEPMDIGSTIPLAKKFORIVHKSIVLILPGANDDEHONKINMNYIEGKRL 495
QY      497      FFAFFLEMAQLH 508
DB      496      FFAFFLEMAQLH 507

RESULT 9
US-10-036-342-57
; Sequence 57, Application US/10036342
; Publication No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenlin
TITLE OF INVENTION: SECURED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C5
CURRENT APPLICATION NUMBER: US/10/036,342
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
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PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/127706
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PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131270
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PRIOR FILING DATE: 1999-05-25
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PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
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PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 57
LENGTH: 507
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-342-57
Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY LLLLLLGGWSSPPPALLEKVFQYIDLHQBEPVQTLKEWVAISDSVQPPRPROELF 76
DB LLLLLLGGWSSPPPALLEKVFQYIDLHQBEPVQTLKEWVAISDSVQPPRPROELF 75
QY RMAVAADTLQRLGAVASVDMGPQOLPDGSLPIPPVILAEISGPTKGTVCYGHLDV 136
DB RMAVAADTLQRLGAVASVDMGPQOLPDGSLPIPPVILAEISGPTKGTVCYGHLDV 135
QY QPADRGDWLTPPYVTEVDGKLYGKATDNKGPVILAMINAVSAPFALEQDLPVNIKFTI 196
DB QPADRGDWLTPPYVTEVDGKLYGKATDNKGPVILAMINAVSAPFALEQDLPVNIKFTI 195
QY EGMERAGSVALELVEKEKDRFFSGVDYVVISDNLMISORKEALTYGTGNSYFMWEVVC 256
DB EGMERAGSVALELVEKEKDRFFSGVDYVVISDNLMISORKEALTYGTGNSYFMWEVVC 255
QY RDQDFHSGTGGILHEPMADLVALLGSLVDSGHLIVPGIYDEVVPLTEEEINTYKAHIL 316
DB RDQDFHSGTGGILHEPMADLVALLGSLVDSGHLIVPGIYDEVVPLTEEEINTYKAHIL 316

Db 256 RDQDHSSTGFGGILHMPMDVLVALLGSLVDSGHLIVPGIYDEVVPLTEELINTYKAITHL 315
Qy 317 DIEEYRNSRVEKEFLPDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
Db 316 DIEEYRNSRVEKEFLPDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375
Qy 377 RLVPMNVSAVKQVTRHLEDVFSKNSNKNVSVTTGLHFWININDTOYLAARRAR 436
Db 376 RLVPMNVSAVKQVTRHLEDVFSKNSNKNVSVTTGLHFWININDTOYLAARRAR 435
Qy 437 TVFGTEPDMIRDSSTIPAKMFQEIYHKSIVLIPLGAVDDGSHSQNEKINRNYIEGTYL 496
Db 436 TVFGTEPDMIRDSSTIPAKMFQEIYHKSIVLIPLGAVDDGSHSQNEKINRNYIEGTYL 495
Qy 497 PAAFFLEMAQLH 508
Db 496 PAAFFLEMAQLH 507

RESULT 10
US-10-036-041-57
Sequence 57, Application US/10036041
Publication No. US20020192751A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C8
CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
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PRIOR FILING DATE: 2001-06-05
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
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PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
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PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80

SEQ ID NO 57
 LENGTH: 507
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-036-041-57

Query Match 96.9%; Score 492; DB 4; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	17	LLLLLEGGMFSSPPPLLEKVFQYIDLHODEFVQTLKEVNAIESDSVQVPPRRQELF	76
DB	16	LLLLLEGGMFSSPPPLLEKVFQYIDLHODEFVQTLKEVNAIESDSVQVPPRRQELF	75
QY	77	RMVAADTLORLARVASVDMGFOQLPDGSLPIPPVILAEGLSDPTKGVCCYGHLDV	136
DB	76	RMVAADTLORLARVASVDMGFOQLPDGSLPIPPVILAEGLSDPTKGVCCYGHLDV	135
QY	137	QPADRGDWLTPVYLTEVDGKLYGRGATDNKGFVLAMINAVSAFRLAEODLPVNIKFI	196
DB	136	QPADRGDWLTPVYLTEVDGKLYGRGATDNKGFVLAMINAVSAFRLAEODLPVNIKFI	195
QY	197	EGMEASVALBELVEKRFESGVDTYVSDNLMISQKKPAITTYGTRGNSYFMEVVC	256
DB	196	EGMEASVALBELVEKRFESGVDTYVSDNLMISQKKPAITTYGTRGNSYFMEVVC	255
QY	257	RDODFHSGTGGILHEPMADLVALGSLVDSGHIIVPGIYDEVVPLTEERINTYKAHL	316
DB	256	RDODFHSGTGGILHEPMADLVALGSLVDSGHIIVPGIYDEVVPLTEERINTYKAHL	315
QY	317	DLEBYRNSRVEKEFLPDTKEIILMLWRYPISLHGIEGAFDEBGTQTVIIGRVIGKFSI	376
DB	316	DLEBYRNSRVEKEFLPDTKEIILMLWRYPISLHGIEGAFDEBGTQTVIIGRVIGKFSI	375
QY	377	RLVPHNVASAVEKQVTHLEDFESKNSNKMVSMVLGLHPWIANIDTQYLAAKAIR	436
DB	376	RLVPHNVASAVEKQVTHLEDFESKNSNKMVSMVLGLHPWIANIDTQYLAAKAIR	435
QY	437	TVFGTEPDMIRDSGTIPAKMFOEIVHKSIVLPLGAVDDGESHONKIRMYITECTKL	496
DB	436	TVFGTEPDMIRDSGTIPAKMFOEIVHKSIVLPLGAVDDGESHONKIRMYITECTKL	495
QY	497	FAAFLEMAQLH 508	
DB	496	FAAFLEMAQLH 507	

RESULT 11
 US-10-035-855-57
 Sequence 57, Application US/10035855
 Publication No. US20030008348A1
 GENERAL INFORMATION:
 APPLICANT: Deanoys, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zhen
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P030R1C4
 CURRENT APPLICATION NUMBER: US/10/035, 855
 CURRENT FILING DATE: 2001-12-26
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/112514
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 PRIOR APPLICATION NUMBER: 60/116843
 PRIOR FILING DATE: 1999-01-22
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 PRIOR FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: 60/125778
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 PRIOR FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: PCT/US99/10733
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 PRIOR APPLICATION NUMBER: PCT/US99/28551
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30720

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/ PRIOR FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: PCT/US00/05601
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
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/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: PCT/US01/17800
/ PRIOR FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: PCT/US01/19692
/ PRIOR FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21066
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 80
/ SEQ ID NO 57
/ LENGTH: 507
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-035-855-57
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Query Match          96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLLERNFSSPPSPALLLEKVFQYIDHODEFVQTLKEMVAISDSVQVPRFRQELF 76
DB 16 LLLLLLERNFSSPPSPALLLEKVFQYIDHODEFVQTLKEMVAISDSVQVPRFRQELF 75
QY 77 RMAVAADLTQRLGARNVAVDMGPGQQLPBGOSLPPIPVILAEIGSDPTGTCFYGHLDV 136
DB 76 RMAVAADLTQRLGARNVAVDMGPGQQLPBGOSLPPIPVILAEIGSDPTGTCFYGHLDV 135
QY 137 OPADRGDGLTTPYVLTVEVDGKLYGRGATDNKGVPVLAMINAVSAPRALEQDLPVNIKFI 196
DB 136 OPADRGDGLTTPYVLTVEVDGKLYGRGATDNKGVPVLAMINAVSAPRALEQDLPVNIKFI 195
QY 197 ESMEEAGSVALBELVEKEKDRFFSGVDYIVISDNIMIQRKPAITYTGRGNSYFMVEYVC 256
DB 196 ESMEEAGSVALBELVEKEKDRFFSGVDYIVISDNIMIQRKPAITYTGRGNSYFMVEYVC 255
QY 257 RQODHSGTFFGGLIHEPMADYVALLGSLVDSGSHLIVPEIYDEVVPLTBEENYTKAHL 316
DB 256 RQODHSGTFFGGLIHEPMADYVALLGSLVDSGSHLIVPEIYDEVVPLTBEENYTKAHL 315
QY 317 DLEERYNSRVRKFLPDTKEIIMLMRYPSLSIHGIEGAPDEPGTKTVIPGRVIGKFSI 376
DB 316 DLEERYNSRVRKFLPDTKEIIMLMRYPSLSIHGIEGAPDEPGTKTVIPGRVIGKFSI 375
QY 377 RLVPNNVSAVEKQVTRHLEDEVFSKRNSNNKVVNTTGLAFWIANIDDTQYLAARAIR 436
DB 376 RLVPNNVSAVEKQVTRHLEDEVFSKRNSNNKVVNTTGLAFWIANIDDTQYLAARAIR 435
QY 437 TVFGTEPDMIRDSGTIPKAKFOELVHKSVULIPGAVDDGSHSQNEKINRWNYLEGYTL 496
DB 436 TVFGTEPDMIRDSGTIPKAKFOELVHKSVULIPGAVDDGSHSQNEKINRWNYLEGYTL 495
QY 497 PAAFFLEMAQLH 508
DB 496 PAAFFLEMAQLH 507
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RESULT 12
US-10-036-214-57
/ Sequence 57, Application US/10036214
/ Publication No. US20030032061A1
/ GENERAL INFORMATION:
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3030R1C11
/ CURRENT APPLICATION NUMBER: US/10/036,214
/ CURRENT FILING DATE: 2001-12-26
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
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 PRIOR APPLICATION NUMBER: PCT/US01/19692
 PRIOR FILING DATE: 2001-06-20
 PRIOR APPLICATION NUMBER: PCT/US01/21066
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: PCT/US01/21735
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 80
 SEQ ID NO 57
 LENGTH: 507
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-036-214-57

Query Match 96.9%; Score 492; DB 4; Length 507;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLEKGMSSSPSPALAEKVFQYIDLHODEFVQTLKEMVAIESDSVQVPRFRQELP 76
 Db 16 LLLLEKGMSSSPSPALAEKVFQYIDLHODEFVQTLKEMVAIESDSVQVPRFRQELP 75
 QY 77 RMAVAADTLQRLGARVAVYDMGPOOLPDGOSLPIPPVILAEISGDPKTKVCFYGLDV 136
 Db 76 RMAVAADTLQRLGARVAVYDMGPOOLPDGOSLPIPPVILAEISGDPKTKVCFYGLDV 135

QY 137 QPADRGDWLTDPYVLTENVGKLYGRGATNKGPLYAMTANVASAFRALBODLPVNTKFI 136
 Db 136 QPADRGDWLTDPYVLTENVGKLYGRGATNKGPLYAMTANVASAFRALBODLPVNTKFI 135
 QY 197 EGMEEAGSVALBELVEKEKDPFSGVDYIVISDNLISORRPAITYGTGNSYFMVEVKC 256
 Db 196 EGMEEAGSVALBELVEKEKDPFSGVDYIVISDNLISORRPAITYGTGNSYFMVEVKC 255
 QY 257 RDDDFHSFTFGGILHEPMADLVALLSGSLVDSGHIIVPGIYDEVVPLTEBEINTYAIHL 316
 Db 256 RDDDFHSFTFGGILHEPMADLVALLSGSLVDSGHIIVPGIYDEVVPLTEBEINTYAIHL 315
 QY 317 DLEERNSSRVEKFLPDTKEELIMHLRYPVSLIHIEGAFDEPRGKTYIPGVICKFSI 376
 Db 316 DLEERNSSRVEKFLPDTKEELIMHLRYPVSLIHIEGAFDEPRGKTYIPGVICKFSI 375
 QY 377 RLVPHNVASAVEKQVTRHLEDVFSKNSNKNVSVTLGLHPWIANIDTQYLAARAIR 436
 Db 376 RLVPHNVASAVEKQVTRHLEDVFSKNSNKNVSVTLGLHPWIANIDTQYLAARAIR 435
 QY 437 TVFGTEPDMIRDGSTIPIAKMFOEIVHKSIVLIPGLAVDDGEHSQNEKINRMVYIGTKY 496
 Db 436 TVFGTEPDMIRDGSTIPIAKMFOEIVHKSIVLIPGLAVDDGEHSQNEKINRMVYIGTKY 495
 QY 497 FAAPFLEMAQLH 508
 Db 496 FAAPFLEMAQLH 507

RESULT 13
 US-10-035-719-57
 Sequence 57, Application US/10035719
 Publication No. US20030036114A1
 GENERAL INFORMATION:
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Abustin L.
 APPLICANT: Pan, James
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3030R1C2
 CURRENT APPLICATION NUMBER: US/10/035,719
 PRIOR FILING DATE: 2001-12-26
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/112514
 PRIOR FILING DATE: 1998-12-15
 PRIOR APPLICATION NUMBER: 60/113300
 PRIOR FILING DATE: 1998-12-22
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 PRIOR APPLICATION NUMBER: 60/114140
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 PRIOR APPLICATION NUMBER: 60/115552
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/116843
 PRIOR FILING DATE: 1999-01-22
 PRIOR APPLICATION NUMBER: 60/125774
 PRIOR FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: 60/125778
 PRIOR FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: 60/125826

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; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
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; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
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; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908, 827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
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; PRIOR FILING DATE: 2000-05-22
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; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: PCT/US01/06520
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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-719-57

Query Match          96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

17 LLLLLLGGMFSSPPPPALLLEKVFQYIDLHODEFVQTLKEWVAIESDSVQVPRPRQELF 76
16 LLLLLLGGMFSSPPPPALLLEKVFQYIDLHODEFVQTLKEWVAIESDSVQVPRPRQELF 75
77 RMMVAADTLQRLGARVASVVMGPOQLPDGQSLPIPPVITLALSGDPTKGYCFGHLDV 136
76 RMMVAADTLQRLGARVASVVMGPOQLPDGQSLPIPPVITLALSGDPTKGYCFGHLDV 135
137 QPADRGDMLTDPYVLTEDGKLYGRGATDNKGPYLAWINAVSAFRALEODLPVNIKFTI 196
136 QPADRGDMLTDPYVLTEDGKLYGRGATDNKGPYLAWINAVSAFRALEODLPVNIKFTI 195
197 EGMEBAGSVALLEELVEKEKDRPFGVDYIVISDNLMTISQRPAITYGTRGNSYFWEVYC 256
196 EGMEBAGSVALLEELVEKEKDRPFGVDYIVISDNLMTISQRPAITYGTRGNSYFWEVYC 255
257 RDOPHSGTGGIILHEPADLVALLSVDSGGHILVGIYDEVVPLTEEBINTYKAHL 316
256 RDQPHSGTGGIILHEPADLVALLSVDSGGHILVGIYDEVVPLTEEBINTYKAHL 315
317 DLEERYNRSRYEKFVDTKEEILMHLNRPYSLSHGIEGAFDEPQTKTIVIGRVIGKFSI 376
316 DLEERYNRSRYEKFVDTKEEILMHLNRPYSLSHGIEGAFDEPQTKTIVIGRVIGKFSI 375
377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWTANIDTQYLAAKRAIR 436
376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSNMVVSMTLGLHPWTANIDTQYLAAKRAIR 435
437 TVFGTEPMTIDGSTIPAKKFORIYKSVYLPLGAVDDEHSONEKINRWNYIEGKTL 496
436 TVFGTEPMTIDGSTIPAKKFORIYKSVYLPLGAVDDEHSONEKINRWNYIEGKTL 495
497 FAAPFLMAQLH 508
496 FAAPFLMAQLH 507

RESULT 14
US-10-036-160-57
; Sequence 57, Application US/10036160
; Publication No. US20030044842A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C3
CURRENT APPLICATION NUMBER: US/10/036,160
PRIOR APPLICATION NUMBER: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
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PRIOR FILING DATE: 1998-12-23
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PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
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PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
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PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 57
LENGTH: 507
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-160-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

17 LLLLLERGMFSSPPPALLEKVFQYIDHODEPVQTLKEMVAIESDSVQVPRFRQELF 76
16 LLLLLERGMFSSPPPALLEKVFQYIDHODEPVQTLKEMVAIESDSVQVPRFRQELF 75
77 RMAVAADTLQRLGKARVASVDMGPQQLPDGQSLPIPVIIAELGSDPTGTCFYGLDV 136
76 RMAVAADTLQRLGKARVASVDMGPQQLPDGQSLPIPVIIAELGSDPTGTCFYGLDV 135
137 QPADRDGWLTDPPYVITEVDGKLYGKATDNKGPVLAMINAVSAPRALFQDLPVNIKFTI 196
136 QPADRDGWLTDPPYVITEVDGKLYGKATDNKGPVLAMINAVSAPRALFQDLPVNIKFTI 195
197 EGMEEAGSVALELVEKEKDRPFSGVDYVITSDNLMISORKRALITGTGNSYPMWEVVC 256
196 EGMEEAGSVALELVEKEKDRPFSGVDYVITSDNLMISORKRALITGTGNSYPMWEVVC 255
257 RQDFHSGTGGIILHEPMADVLALGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHL 316
256 RQDFHSGTGGIILHEPMADVLALGSLVDSSGHILVPGIYDEVVPLTTEEINTYKAHL 315
317 DLEETRNSSRVKFLFDYKEEILMHLWRYPSLSIHGIGAFDEPGTKTYIPGRVIGKFSI 376
316 DLEETRNSSRVKFLFDYKEEILMHLWRYPSLSIHGIGAFDEPGTKTYIPGRVIGKFSI 375

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLRGMSPPSPALLLEKFKQYIDLHODEFVQTLKEMVAIESDSVPVPRROELF 76
DB 16 LLLLLRGMSPPSPALLLEKFKQYIDLHODEFVQTLKEMVAIESDSVPVPRROELF 75
QY 77 RMAVAADTLQRIAGARVAVDMGPQOLPDGQSLPIPVIIAEIGSDPTKGTVCYGLDV 136
DB 76 RMAVAADTLQRIAGARVAVDMGPQOLPDGQSLPIPVIIAEIGSDPTKGTVCYGLDV 135
QY 137 QPADRGDWLTDPYVLTVDGKLYGRGATDNKGVLAMINAVSAFRLBODLVNKEFI 196
DB 136 QPADRGDWLTDPYVLTVDGKLYGRGATDNKGVLAMINAVSAFRLBODLVNKEFI 195
QY 197 EGMEBAGSVLBEIYVEKORFPGVDYIYISDNLMTSQKKPAITYGTRGNSYFMVEVKC 266
DB 196 EGMEBAGSVLBEIYVEKORFPGVDYIYISDNLMTSQKKPAITYGTRGNSYFMVEVKC 265
QY 257 RQDDFSGTGGILHEPMADLVALLGSLVDSGHIIVPGIYDEVPLTESEINTYKAHL 316
DB 256 RQDDFSGTGGILHEPMADLVALLGSLVDSGHIIVPGIYDEVPLTESEINTYKAHL 315
QY 317 DLEBYNNSRVEKFLPDTKEEILMLRWYPSLSIHGIEGAFDEPGTKTVIPGVIGKFSI 376
DB 316 DLEBYNNSRVEKFLPDTKEEILMLRWYPSLSIHGIEGAFDEPGTKTVIPGVIGKFSI 375
QY 377 RLVPHNVSAVEKQVTRHLEDVPSKNSNKMVVSMTLGLHPMIANIDTOYLAARAIR 436
DB 376 RLVPHNVSAVEKQVTRHLEDVPSKNSNKMVVSMTLGLHPMIANIDTOYLAARAIR 435
QY 437 TVEGTSPDMRDGSTPIAKMFOEIVHKSVLLPLGAVDDGESHQNEKINRMVYIGTKL 496
DB 436 TVEGTSPDMRDGSTPIAKMFOEIVHKSVLLPLGAVDDGESHQNEKINRMVYIGTKL 495
QY 497 FFAFLEMAQLH 508
DB 496 FFAFLEMAQLH 507

RESULT 16
US-10-036-150-57
; Sequence 57, Application US/10036150
; Publication No. US20030049734A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyer, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C9
; CURRENT APPLICATION NUMBER: US/10/036.150
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
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; PRIOR APPLICATION NUMBER: 60/113430
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; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
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; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
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; PRIOR APPLICATION NUMBER: 60/127706
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; PRIOR FILING DATE: 2001-03-22
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; PRIOR APPLICATION NUMBER: 09/854280
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; PRIOR FILING DATE: 2001-06-29
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; PRIOR APPLICATION NUMBER: PCT/US00/05601
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; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042


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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-150-57

Query Match      96.9%; Score 492; DB 4; Length 507;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLLLRRGFPSSPPSPALLLEKVFQYIDLHODEFVQTLKEMVAISDSVQVPRRQELF 76
DB 16 LLLLLLRRGFPSSPPSPALLLEKVFQYIDLHODEFVQTLKEMVAISDSVQVPRRQELF 75
QY 77 RMAVAADTLQRLGKRVASVDMGPQQLPDGQSLPIPVVLAELGSDPTGTCFTGHLDV 136
DB 76 RMAVAADTLQRLGKRVASVDMGPQQLPDGQSLPIPVVLAELGSDPTGTCFTGHLDV 135
QY 137 QPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPLYLAWINAVSAPFALEQDLPVNIKFI 196
DB 136 QPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPLYLAWINAVSAPFALEQDLPVNIKFI 195
QY 197 EEMERAGSALBELVEKEKDRFPSSGVYIVISDNMISQRKALITYGTRGNSYFMWEVKC 256
DB 196 EEMERAGSALBELVEKEKDRFPSSGVYIVISDNMISQRKALITYGTRGNSYFMWEVKC 255
QY 257 RQDDFHSSTFGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHL 316
DB 256 RQDDFHSSTFGGILHEPMADLVALLGSLVDSGGHILVPGIYDEVVPLTEEEINTYKAHL 315
QY 317 DLEBYRNSSRVEKFLFDTKERILMLMRYPSLSIHQIEGAFDEPGTKTVIPGRVIGKFSI 376
DB 316 DLEBYRNSSRVEKFLFDTKERILMLMRYPSLSIHQIEGAFDEPGTKTVIPGRVIGKFSI 375
QY 377 RLVPHNNVSAVKEKQVTRHLEDFVSKRNSNKNVSMVTLGLHFWININIDTQYLAAKRAIR 436
DB 376 RLVPHNNVSAVKEKQVTRHLEDFVSKRNSNKNVSMVTLGLHFWININIDTQYLAAKRAIR 435
QY 437 TVFGTEPDMIRDSSTPIAKMFOELVHKSVVLIPIGAVDDGSHSONEKNRNNYIEGTL 496
DB 436 TVFGTEPDMIRDSSTPIAKMFOELVHKSVVLIPIGAVDDGSHSONEKNRNNYIEGTL 495
QY 497 FAAPFLEMAQLH 508
DB 496 FAAPFLEMAQLH 507
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; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C6
; CURRENT APPLICATION NUMBER: US/10/036, 063
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
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; PRIOR FILING DATE: 1999-03-23
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; PRIOR FILING DATE: 1999-04-05
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
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/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 09/644848
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 09/747259
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 09/816744
/ PRIOR FILING DATE: 2001-03-22
/ PRIOR APPLICATION NUMBER: 09/854208
/ PRIOR FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 09/854280
/ PRIOR FILING DATE: 2001-05-10
/ PRIOR APPLICATION NUMBER: 09/874503
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/869599
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: 09/908,827
/ PRIOR FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: PCT/US99/10733
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: PCT/US99/28551
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30720
/ PRIOR FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: PCT/US00/05601
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: 2000-03-02
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: PCT/US00/15264
/ PRIOR FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US00/34956
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: PCT/US01/17800
/ PRIOR FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: PCT/US01/19692
/ PRIOR FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21066
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 80
/ SEQ ID NO 57
/ LENGTH: 507
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-036-063-57

Query Match      96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LLLLLLGGFSSPPPALLEKVFQYIDLHODEFVOTLKEMVAIESDSVQVPRFROELF 76
Db 16 LLLLLLGGFSSPPPALLEKVFQYIDLHODEFVOTLKEMVAIESDSVQVPRFROELF 75
Qy 77 RMAVAADTLQRIQAVASVDMGPPOOLPGQSIPPIPVIIAELIGSDPTKGVCFYGHLDV 136
Db 76 RMAVAADTLQRIQAVASVDMGPPOOLPGQSIPPIPVIIAELIGSDPTKGVCFYGHLDV 135
Qy 137 OPADRDGWLTDPPYVLTVDGKLYGRGATDNKGPTVLAMNAVAFAPLAEODLPPVNIKFTI 196
Db 136 QPADRDGWLTDPPYVLTVDGKLYGRGATDNKGPTVLAMNAVAFAPLAEODLPPVNIKFTI 195
Qy 197 EGMEAGSVALBELVEKEDRPFSSGVYIVISDNLWISQRKPAITYGTRGNSYFMVEVXC 256
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Db 196 EGMEAGSVALBELVEKEDRPFSSGVYIVISDNLWISQRKPAITYGTRGNSYFMVEVXC 255
Qy 257 RDDDFHSGTFGGTILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEBINTYKAHIL 316
Db 256 RDDDFHSGTFGGTILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEBINTYKAHIL 315
Qy 317 DLEEVNNSRVEKFLDPTKEILMHLMRYPSSLIHGIEGAPFEPGKTVIPGVIGKFSI 376
Db 316 DLEEVNNSRVEKFLDPTKEILMHLMRYPSSLIHGIEGAPFEPGKTVIPGVIGKFSI 375
Qy 377 RLVPNNVSAVEKQVTRHLEDVFSKKNSSNKNVSWTLGLHPMIANIDDTQYLAARAIR 436
Db 376 RLVPNNVSAVEKQVTRHLEDVFSKKNSSNKNVSWTLGLHPMIANIDDTQYLAARAIR 435
Qy 437 TVFGTEPDMIRDGSTPIAKMFOELVHKSVLLPLGAVDDGHSQNEKINRMVIEGTXL 496
Db 436 TVFGTEPDMIRDGSTPIAKMFOELVHKSVLLPLGAVDDGHSQNEKINRMVIEGTXL 495
Qy 497 FAAFLEMAQLH 508
Db 496 FAAFLEMAQLH 507

RESULT 18
US-10-035-977-57
/ Sequence 57, Application US/10035977
/ Publication No. US20030134327A1
/ GENERAL INFORMATION:
/ APPLICANT: Deenoyere, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Aubstin L.
/ APPLICANT: Pan, James
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3030R1C10
/ CURRENT APPLICATION NUMBER: US/10/035,977
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/112514
/ PRIOR FILING DATE: 1998-12-15
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/ PRIOR APPLICATION NUMBER: 60/113621
/ PRIOR FILING DATE: 1998-12-23
/ PRIOR APPLICATION NUMBER: 60/114140
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/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: 60/127035
/ PRIOR FILING DATE: 1999-03-31
/ PRIOR APPLICATION NUMBER: 60/127706
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: 60/129122
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PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-04
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PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
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PRIOR APPLICATION NUMBER: 09/816744
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PRIOR APPLICATION NUMBER: 09/854208
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PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 57
LENGTH: 507
TYPE: PRT
ORGANISM: Homo Sapien
US-10-035-977-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

17 LLLLLERGMFSSPPSPALLLEKVFQYIDLHODEFQYTLKEMVALESQVQVPRRQELF 76
16 LLLLLERGMFSSPPSPALLLEKVFQYIDLHODEFQYTLKEMVALESQVQVPRRQELF 75
77 RMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPVYTLAELGSDPTKGVCFYGHLDV 136
76 RMAVAADTLQRLGARVASVDMGPOQLPDGQSLPIPVYTLAELGSDPTKGVCFYGHLDV 135
137 QPADRGDGLTDPYVLTEDGKLYGRGATDNKGPVLAWINAVSAPRALEODLPVNIKFI 196
136 QPADRGDGLTDPYVLTEDGKLYGRGATDNKGPVLAWINAVSAPRALEODLPVNIKFI 195
197 EGMEBAGSVALLELVEKEKDRFFSGVDYIVSDNLMISQRPATTYGTRGNSYFMAVEYKC 256
196 EGMEBAGSVALLELVEKEKDRFFSGVDYIVSDNLMISQRPATTYGTRGNSYFMAVEYKC 255
257 RDQDFHSGTGGIILHEPMADLVALGSLVDSGHIIVPGIYDEVVPLTBEINITYKAHL 316
256 RDQDFHSGTGGIILHEPMADLVALGSLVDSGHIIVPGIYDEVVPLTBEINITYKAHL 315
317 DLEERYNSRVEKFLPDKKEILMLMRYPSSLIHGIGARDEBGTQVIRGVYKFSI 376
316 DLEERYNSRVEKFLPDKKEILMLMRYPSSLIHGIGARDEBGTQVIRGVYKFSI 375
377 RLVPMMVSAVEKQVTRLLEDFVSKRNSNMKVYSMTLGLHPWLANIDDTQYLAARAIR 436
376 RLVPMMVSAVEKQVTRLLEDFVSKRNSNMKVYSMTLGLHPWLANIDDTQYLAARAIR 435
437 TVFGTEPMDIGSTIPLAKKFOEIVKSVTLPLGAVDDGSHQNEKINFWYIEGTYL 496
436 TVFGTEPMDIGSTIPLAKKFOEIVKSVTLPLGAVDDGSHQNEKINFWYIEGTYL 495
497 FAAPFLEMAQLH 508
496 FAAPFLEMAQLH 507

RESULT 19
US-10-275-107-68
Sequence 68, Application US/10275107
Publication No. US20040063107A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY D.
APPLICANT: WHYTE, DAVID
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: MANNING, GERRARD
APPLICANT: CAENEPEEL, SEAN R.
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1479
CURRENT APPLICATION NUMBER: US/10/275,107
CURRENT FILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: PCT/US01/14431
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/201,879
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 68
LENGTH: 507
TYPE: PRT
ORGANISM: Homo sapiens
US-10-275-107-68

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLEKGMFSSPPALLEKVFQYIDHODEFVQTLKEMVAIESDSVQVPRFRQELF 76
DB 16 LLLLEKGMFSSPPALLEKVFQYIDHODEFVQTLKEMVAIESDSVQVPRFRQELF 75
QY 77 RMAVAADTLORIGARVASVDMGPOQLPDGOSLPPIPVVILAEIGSPPTGTCFYGHLDV 136
DB 76 RMAVAADTLORIGARVASVDMGPOQLPDGOSLPPIPVVILAEIGSPPTGTCFYGHLDV 135
QY 137 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLAEODLPVNIKFII 196
DB 136 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLAEODLPVNIKFII 195
QY 197 EGMEEAGSVALBELVEKEKORFPGSVYIYISDNLMISORKPALITGTGNSYFMVEVKC 256
DB 196 EGMEEAGSVALBELVEKEKORFPGSVYIYISDNLMISORKPALITGTGNSYFMVEVKC 255
QY 257 RQDDFHSGTGGILHEPMADLVALLGSLVDSGHLVPGIYDEVPLTEEBINTYKAHL 316
DB 256 RQDDFHSGTGGILHEPMADLVALLGSLVDSGHLVPGIYDEVPLTEEBINTYKAHL 315
QY 317 DLEBYNSSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIIPGRVIGKFSI 376
DB 316 DLEBYNSSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIIPGRVIGKFSI 375
QY 377 RLVPHNNSAVKQVTRHLEDVFSKNSNKNVVSMTGLHPWIANIDTQYLAARAIR 436
DB 376 RLVPHNNSAVKQVTRHLEDVFSKNSNKNVVSMTGLHPWIANIDTQYLAARAIR 435
QY 437 TVFGTEPDMIRDSSTPIAKMFOEIVKSVVLLPLGAVDDGSHSONEKINRMNYIGTKL 496
DB 436 TVFGTEPDMIRDSSTPIAKMFOEIVKSVVLLPLGAVDDGSHSONEKINRMNYIGTKL 495
QY 497 PAAFLFEMAQLH 508
DB 496 PAAFLFEMAQLH 507

RESULT 20

US-10-884-091-57
Sequence 57, Application US/10884091
Publication No. US20040265966A1
GENERAL INFORMATION:
APPLICANT: Deenoyere, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pen, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: P3030R1C1C1
CURRENT APPLICATION NUMBER: US/10/884, 091
CURRENT FILING DATE: 2004-07-01
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 57
LENGTH: 507
TYPE: PRT
ORGANISM: Homo Sapien
US-10-884-091-57

Query Match 96.9%; Score 492; DB 5; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLLLEKGMFSSPPALLEKVFQYIDHODEFVQTLKEMVAIESDSVQVPRFRQELF 76
DB 16 LLLLEKGMFSSPPALLEKVFQYIDHODEFVQTLKEMVAIESDSVQVPRFRQELF 75
QY 77 RMAVAADTLORIGARVASVDMGPOQLPDGOSLPPIPVVILAEIGSPPTGTCFYGHLDV 136
DB 76 RMAVAADTLORIGARVASVDMGPOQLPDGOSLPPIPVVILAEIGSPPTGTCFYGHLDV 135
QY 137 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLAEODLPVNIKFII 196
DB 136 QPADRGDGLTDPYVLTVEVDGKLYGRGATDNKGPVLAMINAVSAFRLAEODLPVNIKFII 195
QY 197 EGMEEAGSVALBELVEKEKORFPGSVYIYISDNLMISORKPALITGTGNSYFMVEVKC 256
DB 196 EGMEEAGSVALBELVEKEKORFPGSVYIYISDNLMISORKPALITGTGNSYFMVEVKC 255
QY 257 RQDDFHSGTGGILHEPMADLVALLGSLVDSGHLVPGIYDEVPLTEEBINTYKAHL 316
DB 256 RQDDFHSGTGGILHEPMADLVALLGSLVDSGHLVPGIYDEVPLTEEBINTYKAHL 315
QY 317 DLEBYNSSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIIPGRVIGKFSI 376
DB 316 DLEBYNSSRVEKFLPDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKVIIPGRVIGKFSI 375
QY 377 RLVPHNNSAVKQVTRHLEDVFSKNSNKNVVSMTGLHPWIANIDTQYLAARAIR 436
DB 376 RLVPHNNSAVKQVTRHLEDVFSKNSNKNVVSMTGLHPWIANIDTQYLAARAIR 435
QY 437 TVFGTEPDMIRDSSTPIAKMFOEIVKSVVLLPLGAVDDGSHSONEKINRMNYIGTKL 496
DB 436 TVFGTEPDMIRDSSTPIAKMFOEIVKSVVLLPLGAVDDGSHSONEKINRMNYIGTKL 495
QY 497 PAAFLFEMAQLH 508
DB 496 PAAFLFEMAQLH 507

RESULT 21

US-09-791-378-674
Sequence 674, Application US/09791378
Patent No. US20020142303A1
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999
CURRENT APPLICATION NUMBER: US/09/791,378

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/ CURRENT FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 09/750,395
/ PRIOR FILING DATE: 2000-12-28
/ NUMBER OF SEQ ID NOS: 677
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 674
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (70)..(70)
/ OTHER INFORMATION: Xaa = Ile or Leu
US-09-791-378-674
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Query Match      84.4%; Score 429; DB 3; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 78 MAAVAADTLQRLGARVASVDMGPQQLPDGSLPIPPVILAEISGDPYKTCFYGHLDVQ 137
DB 71 MAAVAADTLQRLGARVASVDMGPQQLPDGSLPIPPVILAEISGDPYKTCFYGHLDVQ 130
QY 138 PADRDGMLTDPYVLTVDGKLYGRGATDNKGPVLAMINAVSAFRALBODLPVNIKFTIE 197
DB 131 PADRDGMLTDPYVLTVDGKLYGRGATDNKGPVLAMINAVSAFRALBODLPVNIKFTIE 190
QY 198 GMEBAGSVALBELVEKEKDRFSGVDYIVISDNLMISQRKPAITYGTGNSYFMWEVKCR 257
DB 191 GMEBAGSVALBELVEKEKDRFSGVDYIVISDNLMISQRKPAITYGTGNSYFMWEVKCR 250
QY 258 DDDFSGTGGGILHEPMADLVALLGSLVDSGSHILVPGIYDEVVPLTEEBINTYKAIHLD 317
DB 251 DDDFSGTGGGILHEPMADLVALLGSLVDSGSHILVPGIYDEVVPLTEEBINTYKAIHLD 310
QY 318 LEEYNSRSVEKFLPDTKEEILMLHMRYPSTLHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
DB 311 LEEYNSRSVEKFLPDTKEEILMLHMRYPSTLHGIEGAFDEPGTKTVIPGRVIGKFSIR 370
QY 378 LVPHNNAVAVEKQVTRHLEDVFSKNSSNKRVVSWTLGLHPMIANIDTQYLAARKAIRT 437
DB 371 LVPHNNAVAVEKQVTRHLEDVFSKNSSNKRVVSWTLGLHPMIANIDTQYLAARKAIRT 430
QY 438 VFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTCLF 497
DB 431 VFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTCLF 490
QY 498 AAFLEMAQ 506
DB 491 AAFLEMAQ 499
```

```
RESULT 22
US-09-791-393-2
/ Sequence 2, Application US/09791393
/ Publication No. US20030032200A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Parekh, Rajesh Bhikhu
/ TITLE OF INVENTION: Proteins, Genes and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
/ FILE REFERENCE: 2543-1-001 N1
/ CURRENT FILING DATE: US/09/791,393
/ PRIOR FILING DATE: 2002-01-02
/ EARLIER APPLICATION NUMBER: GB 0004412.3
/ PRIOR FILING DATE: 2000-02-24
/ EARLIER APPLICATION NUMBER: GB 0030050.9
/ EARLIER FILING DATE: 2000-12-08
/ EARLIER APPLICATION NUMBER: US 60/254,830
/ EARLIER FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 308
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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: homo sapien
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1)....(501)
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-09-791-393-2
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Query Match      84.4%; Score 429; DB 3; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 78 MAAVAADTLQRLGARVASVDMGPQQLPDGSLPIPPVILAEISGDPYKTCFYGHLDVQ 137
DB 71 MAAVAADTLQRLGARVASVDMGPQQLPDGSLPIPPVILAEISGDPYKTCFYGHLDVQ 130
QY 138 PADRDGMLTDPYVLTVDGKLYGRGATDNKGPVLAMINAVSAFRALBODLPVNIKFTIE 197
DB 131 PADRDGMLTDPYVLTVDGKLYGRGATDNKGPVLAMINAVSAFRALBODLPVNIKFTIE 190
QY 198 GMEBAGSVALBELVEKEKDRFSGVDYIVISDNLMISQRKPAITYGTGNSYFMWEVKCR 257
DB 191 GMEBAGSVALBELVEKEKDRFSGVDYIVISDNLMISQRKPAITYGTGNSYFMWEVKCR 250
QY 258 DDDFSGTGGGILHEPMADLVALLGSLVDSGSHILVPGIYDEVVPLTEEBINTYKAIHLD 317
DB 251 DDDFSGTGGGILHEPMADLVALLGSLVDSGSHILVPGIYDEVVPLTEEBINTYKAIHLD 310
QY 318 LEEYNSRSVEKFLPDTKEEILMLHMRYPSTLHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
DB 311 LEEYNSRSVEKFLPDTKEEILMLHMRYPSTLHGIEGAFDEPGTKTVIPGRVIGKFSIR 370
QY 378 LVPHNNAVAVEKQVTRHLEDVFSKNSSNKRVVSWTLGLHPMIANIDTQYLAARKAIRT 437
DB 371 LVPHNNAVAVEKQVTRHLEDVFSKNSSNKRVVSWTLGLHPMIANIDTQYLAARKAIRT 430
QY 438 VFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTCLF 497
DB 431 VFGTEPDMIRDSSTPIAKMFOEIVHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTCLF 490
QY 498 AAFLEMAQ 506
DB 491 AAFLEMAQ 499
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RESULT 23
US-09-791-389-2
/ Sequence 2, Application US/09791389
/ Publication No. US20030032773A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Rohlff, Christian
/ APPLICANT: Terrett, Jonathan Alexander
/ TITLE OF INVENTION: Proteins, Genes and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
/ FILE REFERENCE: 2543-1-001 N2
/ CURRENT FILING DATE: US/09/791,389
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: GB 0004412.3
/ PRIOR FILING DATE: 2000-02-24
/ EARLIER APPLICATION NUMBER: GB 0030050.9
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/254,830
/ EARLIER FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
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LENGTH: 501
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(501)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-791-389-2

Query Match 84.4%; Score 429; DB 3; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MMAVAADTLQRLGARVASVDMGPOOLPDGQSLPIPPVILAEISDPTKGYCFYGHLDVQ 137
DB 71 MMAVAADTLQRLGARVASVDMGPOOLPDGQSLPIPPVILAEISDPTKGYCFYGHLDVQ 130
QY 138 PADRGDMLTDPVYLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPNVNIKFTIE 197
DB 131 PADRGDMLTDPVYLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPNVNIKFTIE 190
QY 198 GMEBAGSVALBEIYEKEDRPFSGVDYIVISDNLMISQRKAITTYGRGNSYFWEVYKCR 257
DB 191 GMEBAGSVALBEIYEKEDRPFSGVDYIVISDNLMISQRKAITTYGRGNSYFWEVYKCR 250
QY 258 DDPHSGTFFGILHEPMADLVALLSGSLVDSGHLVPGIYDEVVPLTEEINTYKAIHLD 317
DB 251 DDPHSGTFFGILHEPMADLVALLSGSLVDSGHLVPGIYDEVVPLTEEINTYKAIHLD 310
QY 318 LEEYRNSRVEKFLPTKEEILMLMRYPSLSIHGEGAFDEPGTKTVIPGRVIKFSIR 377
DB 311 LEEYRNSRVEKFLPTKEEILMLMRYPSLSIHGEGAFDEPGTKTVIPGRVIKFSIR 370
QY 378 LVPHMNVSAVEKQVTRLIEDVFSKRNSNKMVSMTLGLHPWTANIDDTQYLAAKAIRT 437
DB 371 LVPHMNVSAVEKQVTRLIEDVFSKRNSNKMVSMTLGLHPWTANIDDTQYLAAKAIRT 430
QY 438 VFGTEPMDIRDGSTITPAKMFQEIYHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTKLF 497
DB 431 VFGTEPMDIRDGSTITPAKMFQEIYHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTKLF 490
QY 498 AAFFLEMAQ 506
DB 491 AAFFLEMAQ 499

RESULT 24
US-09-791-377-674
Sequence 674, Application US/09791377
Publication No. US20040110938A1
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 9195-060-999
CURRENT APPLICATION NUMBER: US/09/791,377
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: PatentIn version 3.0
SEQ ID NO 674
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (70)...(70)
OTHER INFORMATION: Xaa = Ile or Leu
US-09-791-377-674

Query Match 84.4%; Score 429; DB 3; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 MMAVAADTLQRLGARVASVDMGPOOLPDGQSLPIPPVILAEISDPTKGYCFYGHLDVQ 137
DB 71 MMAVAADTLQRLGARVASVDMGPOOLPDGQSLPIPPVILAEISDPTKGYCFYGHLDVQ 130
QY 138 PADRGDMLTDPVYLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPNVNIKFTIE 197
DB 131 PADRGDMLTDPVYLTEVDGKLYGRGATDNKGPVLAMINAVSAFRALEQDLPNVNIKFTIE 190
QY 198 GMEBAGSVALBEIYEKEDRPFSGVDYIVISDNLMISQRKAITTYGRGNSYFWEVYKCR 257
DB 191 GMEBAGSVALBEIYEKEDRPFSGVDYIVISDNLMISQRKAITTYGRGNSYFWEVYKCR 250
QY 258 DDPHSGTFFGILHEPMADLVALLSGSLVDSGHLVPGIYDEVVPLTEEINTYKAIHLD 317
DB 251 DDPHSGTFFGILHEPMADLVALLSGSLVDSGHLVPGIYDEVVPLTEEINTYKAIHLD 310
QY 318 LEEYRNSRVEKFLPTKEEILMLMRYPSLSIHGEGAFDEPGTKTVIPGRVIKFSIR 377
DB 311 LEEYRNSRVEKFLPTKEEILMLMRYPSLSIHGEGAFDEPGTKTVIPGRVIKFSIR 370
QY 378 LVPHMNVSAVEKQVTRLIEDVFSKRNSNKMVSMTLGLHPWTANIDDTQYLAAKAIRT 437
DB 371 LVPHMNVSAVEKQVTRLIEDVFSKRNSNKMVSMTLGLHPWTANIDDTQYLAAKAIRT 430
QY 438 VFGTEPMDIRDGSTITPAKMFQEIYHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTKLF 497
DB 431 VFGTEPMDIRDGSTITPAKMFQEIYHKSIVLLPLGAVDDGSHSONEKINRMNYIEGTKLF 490
QY 498 AAFFLEMAQ 506
DB 491 AAFFLEMAQ 499

RESULT 25
US-10-369-022-54
Sequence 54, Application US/10369022
Publication No. US20030203847A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
FILE REFERENCE: M102-027P1RNMNIM
CURRENT APPLICATION NUMBER: US/10/369,022
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/387,536
PRIOR FILING DATE: 2002-06-10
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 54
 LENGTH: 508
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-369-022-54

Query Match 46.3%; Score 235; DB 4; Length 508;
 Best Local Similarity 100.0%; Pred. No. 7.5e-212;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 MADVLALLSGSLVDSGSHILVPGIYDEVVPLTEEEINTYKAIHDLDEYRNSSVKEFLPD 333
 DB 274 MADVLALLSGSLVDSGSHILVPGIYDEVVPLTEEEINTYKAIHDLDEYRNSSVKEFLPD 333
 QY 334 TKEEILMHLMRYPSSLIHGIEGAFDEPGTKTVIPGVIGKFSIRLVPHNVSAVEKQVTR 393
 DB 334 TKEEILMHLMRYPSSLIHGIEGAFDEPGTKTVIPGVIGKFSIRLVPHNVSAVEKQVTR 393
 QY 394 HLEDVFSKNSKSNKVMVSMTLGHPWIANIDTQYLAARAIITVTGTEPDMTRDGSITP 453
 DB 394 HLEDVFSKNSKSNKVMVSMTLGHPWIANIDTQYLAARAIITVTGTEPDMTRDGSITP 453
 QY 454 IAKMPEIYHKSIVLPLGAVDDGESHONEKINRMVYIGSTKLEAFPLEMAQLH 508
 DB 454 IAKMPEIYHKSIVLPLGAVDDGESHONEKINRMVYIGSTKLEAFPLEMAQLH 508

RESULT 26
 US-10-296-115-1427
 Sequence 1427, Application US/10296115
 Publication No. US20040053248A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq Inc
 TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
 FILE REFERENCE: 784PCT
 CURRENT APPLICATION NUMBER: US/10/296,115
 PRIOR FILING DATE: 2002-11-18
 PRIOR APPLICATION NUMBER: US09/488,725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US09/552,317
 PRIOR FILING DATE: 2000-04-25
 NUMBER OF SEQ ID NOS: 1478
 SEQ ID NO 1427
 LENGTH: 133
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-296-115-1427

Query Match 24.8%; Score 126; DB 4; Length 133;
 Best Local Similarity 100.0%; Pred. No. 7.1e-110;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLLAVLILLLERGMFSSPPPALLEKVFQYIDLDHODEFVOTLKEMWAI 60
 DB 8 MDPKLGMAASLLAVLILLLERGMFSSPPPALLEKVFQYIDLDHODEFVOTLKEMWAI 67
 QY 61 ESDSVQVPRFRGELFRMAVAADTLQRLGARVAVSDMGPOQLPDQSLPIPPVILAEIG 120
 DB 68 ESDSVQVPRFRGELFRMAVAADTLQRLGARVAVSDMGPOQLPDQSLPIPPVILAEIG 127
 QY 121 SDPTKG 126
 DB 128 SDPTKG 133

RESULT 27
 US-10-264-237-2057
 Sequence 2057, Application US/10264237
 Publication No. US20040009491A1
 GENERAL INFORMATION:
 APPLICANT: Bitse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PA31P1
 CURRENT APPLICATION NUMBER: US/10/264,237
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: PCT/US01/16450
 PRIOR FILING DATE: 2001-05-18
 PRIOR APPLICATION NUMBER: US 60/205,515
 PRIOR FILING DATE: 2000-05-19
 NUMBER OF SEQ ID NOS: 2876
 SOFTWARE: PatentIn Ver. 3.1
 SEQ ID NO 2057
 LENGTH: 316
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-264-237-2057

Query Match 19.7%; Score 100; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.4e-85;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 EKEKDPFSGVDYIVISNLWISQKPAITYGTGRNSYFMWEVKCRDDPFHSGTGGILH 271
 DB 189 EKEKDPFSGVDYIVISNLWISQKPAITYGTGRNSYFMWEVKCRDDPFHSGTGGILH 248
 QY 272 EPMADVLALLSGSLVDSGSHILVPGIYDEVVPLTEEEINTY 311
 DB 249 EPMADVLALLSGSLVDSGSHILVPGIYDEVVPLTEEEINTY 288

RESULT 28
 US-10-450-763-32013
 Sequence 32013, Application US/10450763
 Publication No. US20050196754A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 FILE REFERENCE: 790CIP3/US
 CURRENT APPLICATION NUMBER: US/10/450,763
 PRIOR FILING DATE: 2003-06-11
 PRIOR APPLICATION NUMBER: PCT/US01/08631
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 09/540,217
 PRIOR FILING DATE: 2000-03-31
 PRIOR APPLICATION NUMBER: 09/649,167
 PRIOR FILING DATE: 2000-08-23
 NUMBER OF SEQ ID NOS: 60736
 SOFTWARE: Custom
 SEQ ID NO 32013
 LENGTH: 100
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(100)
 OTHER INFORMATION: Xaa = X or * as defined in Table 2
 US-10-450-763-32013

Query Match 10.6%; Score 54; DB 5; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.8e-42;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MAASLLAVLILLLERGMFSSPPPALLEKVFQYIDLDHODEFVOTLKEMWAI 61
 DB 1 MAASLLAVLILLLERGMFSSPPPALLEKVFQYIDLDHODEFVOTLKEMWAI 54

RESULT 29
 US-10-450-763-32012
 Sequence 32012, Application US/10450763
 Publication No. US20050196754A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

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; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 32012
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-32012

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Query Match 7.3%; Score 37; DB 5; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.1e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 17 LLLLEGRMSSPPSPALLEKVFQYIDLHODEFVQT 53
DB 62 LLLLEGRMSSPPSPALLEKVFQYIDLHODEFVQT 98

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RESULT 30
US-09-791-378-199
; Sequence 199, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 199
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-199

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Query Match 3.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 56 EWVAIESDSVQPVPR 70
DB 1 EWVAIESDSVQPVPR 15

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Search completed: March 30, 2006, 09:16:19
Job time : 172 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 30, 2006, 09:13:38 ; Search time 24 Seconds
(without alignments)
644.354 Million cell updates/sec

Title: US-10-849-979-139

Perfect score: 508

Sequence: 1 MDPKLGKRMASLAVLLLL.....NYIEGTFLFAFLFMAQLH 508

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Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.8	209	6	US-10-467-657-4066 Sequence 4066, App
2	9	1.8	475	6	US-10-878-556A-115 Sequence 115, App
3	9	1.8	497	7	US-11-087-099-5884 Sequence 5884, App
4	8	1.6	78	7	US-11-123-896-278 Sequence 278, App
5	8	1.6	82	7	US-11-123-896-56 Sequence 56, App
6	8	1.6	110	7	US-11-087-099-8542 Sequence 8542, App
7	8	1.6	114	7	US-11-087-099-2900 Sequence 2900, App
8	8	1.6	277	7	US-11-140-416-34 Sequence 34, App
9	8	1.6	293	7	US-11-096-568A-12504 Sequence 12504, App
10	8	1.6	578	7	US-11-037-243-100 Sequence 100, App
11	8	1.6	579	7	US-11-096-568A-20038 Sequence 20038, App
12	8	1.6	852	6	US-10-645-441-15 Sequence 15, App
13	8	1.6	852	6	US-10-725-475-7 Sequence 7, App
14	8	1.6	852	7	US-11-050-804-6 Sequence 6, App
15	8	1.6	999	7	US-11-113-424-36 Sequence 36, App
16	8	1.6	36	6	US-10-517-696-137 Sequence 137, App
17	7	1.4	79	7	US-11-123-896-468 Sequence 468, App
18	7	1.4	86	6	US-10-475-075-175 Sequence 175, App
19	7	1.4	86	6	US-10-475-075-460 Sequence 460, App
20	7	1.4	86	6	US-11-096-568A-13143 Sequence 13143, App
21	7	1.4	99	7	US-11-176-951-11 Sequence 11, App
22	7	1.4	101	6	US-10-485-788A-775 Sequence 775, App
23	7	1.4	101	7	US-11-053-076-157 Sequence 157, App
24	7	1.4	129	6	US-10-475-075-242 Sequence 242, App
25	7	1.4	129	6	US-10-475-075-243 Sequence 243, App

26	7	1.4	129	6	US-10-475-075-513 Sequence 513, App
27	7	1.4	133	6	US-10-644-807-297 Sequence 297, App
28	7	1.4	134	7	US-11-096-568A-11303 Sequence 11303, App
29	7	1.4	160	7	US-11-096-568A-22510 Sequence 22510, App
30	7	1.4	161	6	US-10-467-657-2842 Sequence 2842, App
31	7	1.4	165	7	US-11-096-568A-22509 Sequence 22509, App
32	7	1.4	190	6	US-10-131-826A-158 Sequence 158, App
33	7	1.4	190	6	US-10-973-115B-158 Sequence 158, App
34	7	1.4	212	7	US-11-096-568A-21456 Sequence 21456, App
35	7	1.4	217	6	US-10-821-234-1568 Sequence 1568, App
36	7	1.4	217	7	US-11-080-991-58 Sequence 58, App
37	7	1.4	217	7	US-11-206-746-2 Sequence 2, App
38	7	1.4	242	6	US-10-063-703-136 Sequence 136, App
39	7	1.4	242	7	US-11-102-240-136 Sequence 136, App
40	7	1.4	242	7	US-11-080-991-30 Sequence 30, App
41	7	1.4	242	7	US-11-103-195-136 Sequence 136, App
42	7	1.4	253	6	US-10-821-234-865 Sequence 2, App
43	7	1.4	254	7	US-11-224-076-2 Sequence 2, App
44	7	1.4	262	7	US-11-087-099-8793 Sequence 8793, App
45	7	1.4	264	7	US-11-096-568A-21455 Sequence 21455, App
46	7	1.4	273	6	US-10-895-561-917 Sequence 917, App
47	7	1.4	295	7	US-11-096-568A-18354 Sequence 18354, App
48	7	1.4	297	7	US-11-096-568A-18353 Sequence 18353, App
49	7	1.4	301	6	US-10-055-877-124 Sequence 124, App
50	7	1.4	301	6	US-10-055-877-261 Sequence 261, App
51	7	1.4	301	7	US-11-000-463-280 Sequence 280, App
52	7	1.4	301	7	US-11-000-463-752 Sequence 752, App
53	7	1.4	301	7	US-11-087-177-35 Sequence 35, App
54	7	1.4	301	7	US-11-087-177-37 Sequence 37, App
55	7	1.4	319	7	US-11-096-568A-18352 Sequence 18352, App
56	7	1.4	320	7	US-11-150-758-2 Sequence 2, App
57	7	1.4	328	6	US-10-131-826A-364 Sequence 364, App
58	7	1.4	328	6	US-10-973-115B-364 Sequence 364, App
59	7	1.4	329	7	US-11-096-568A-5471 Sequence 5471, App
60	7	1.4	329	7	US-11-096-568A-7712 Sequence 7712, App
61	7	1.4	330	7	US-11-087-099-612 Sequence 612, App
62	7	1.4	330	7	US-11-096-568A-7711 Sequence 7711, App
63	7	1.4	339	7	US-11-096-568A-30912 Sequence 30912, App
64	7	1.4	340	7	US-11-096-568A-7710 Sequence 7710, App
65	7	1.4	344	7	US-11-096-568A-18344 Sequence 18344, App
66	7	1.4	346	7	US-11-172-740-1221 Sequence 1221, App
67	7	1.4	347	7	US-11-172-740-1223 Sequence 1223, App
68	7	1.4	348	7	US-11-096-568A-30911 Sequence 30911, App
69	7	1.4	351	7	US-11-096-568A-10873 Sequence 10873, App
70	7	1.4	359	7	US-11-055-822-842 Sequence 842, App
71	7	1.4	362	7	US-11-096-568A-30910 Sequence 30910, App
72	7	1.4	371	6	US-10-595-561-572 Sequence 572, App
73	7	1.4	377	7	US-11-096-568A-12688 Sequence 12688, App
74	7	1.4	381	7	US-11-096-568A-12687 Sequence 12687, App
75	7	1.4	401	6	US-10-055-877-77 Sequence 77, App
76	7	1.4	413	7	US-11-096-568A-20771 Sequence 20771, App
77	7	1.4	419	7	US-11-172-740-744 Sequence 744, App
78	7	1.4	429	7	US-11-087-099-5975 Sequence 5975, App
79	7	1.4	446	7	US-11-096-568A-20810 Sequence 20810, App
80	7	1.4	457	7	US-11-096-568A-20809 Sequence 20809, App
81	7	1.4	461	6	US-10-509-464-77 Sequence 77, App
82	7	1.4	465	7	US-11-087-099-8829 Sequence 8829, App
83	7	1.4	469	7	US-11-096-568A-6976 Sequence 6976, App
84	7	1.4	475	6	US-10-509-464-8 Sequence 8, App
85	7	1.4	510	7	US-11-194-246-442 Sequence 442, App
86	7	1.4	526	6	US-10-467-657-6754 Sequence 6754, App
87	7	1.4	534	7	US-11-096-568A-14686 Sequence 14686, App
88	7	1.4	544	7	US-11-087-099-5596 Sequence 5596, App
89	7	1.4	557	7	US-11-072-511-2707 Sequence 2707, App
90	7	1.4	569	7	US-11-096-568A-6975 Sequence 6975, App
91	7	1.4	597	6	US-10-884-730-381 Sequence 381, App
92	7	1.4	598	7	US-11-096-568A-6974 Sequence 6974, App
93	7	1.4	615	7	US-11-198-819-16 Sequence 16, App
94	7	1.4	615	7	US-11-198-819-18 Sequence 18, App
95	7	1.4	642	6	US-10-131-826A-370 Sequence 370, App
96	7	1.4	642	6	US-10-973-115B-370 Sequence 370, App
97	7	1.4	645	7	US-11-096-568A-19117 Sequence 19117, App
98	7	1.4	648	7	US-11-096-568A-19116 Sequence 19116, App

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99 7 1.4 711 7 US-11-096-568A-19115 Sequence 19115, A
100 7 1.4 792 7 US-11-103-957-25 Sequence 25, App1
101 7 1.4 829 6 US-10-644-807-209 Sequence 209, App1
102 7 1.4 857 7 US-11-096-568A-24558 Sequence 24558, A
103 7 1.4 858 7 US-11-087-099-11449 Sequence 11449, A
104 7 1.4 860 7 US-11-087-099-6246 Sequence 6246, App
105 7 1.4 867 7 US-11-096-568A-24557 Sequence 24557, A
106 7 1.4 884 7 US-11-098-686-11426 Sequence 11426, A
107 7 1.4 903 7 US-11-096-568A-24556 Sequence 24556, A
108 7 1.4 997 7 US-11-080-991-50 Sequence 50, App1
109 7 1.4 1857 6 US-10-055-877-252 Sequence 252, App
110 7 1.4 2084 6 US-10-055-877-73 Sequence 73, App1
111 7 1.4 2107 6 US-10-995-561-827 Sequence 827, App
112 7 1.4 2109 6 US-10-055-877-251 Sequence 251, App
113 7 1.4 2186 7 US-11-096-568A-28283 Sequence 28283, A
114 7 1.4 2199 7 US-11-096-568A-28282 Sequence 28282, A
115 7 1.4 2301 7 US-11-096-568A-28281 Sequence 28281, A
116 7 1.4 2480 6 US-10-995-561-825 Sequence 825, App
117 7 1.4 3116 6 US-10-995-561-826 Sequence 826, App
118 7 1.2 8 7 US-11-045-024-1669 Sequence 1669, App
119 7 1.2 8 7 US-11-045-024-9615 Sequence 9615, App
120 7 1.2 9 7 US-11-045-024-1881 Sequence 1881, App
121 7 1.2 9 7 US-11-045-024-5335 Sequence 5335, App
122 7 1.2 9 7 US-11-045-024-9622 Sequence 9622, App
123 7 1.2 9 7 US-11-033-039-883 Sequence 883, App
124 7 1.2 10 7 US-11-045-024-2105 Sequence 2105, App
125 7 1.2 10 7 US-11-045-024-4631 Sequence 4631, App
126 7 1.2 10 7 US-11-045-024-9629 Sequence 9629, App
127 7 1.2 10 7 US-11-254-419-29 Sequence 29, App1
128 7 1.2 11 7 US-11-045-024-2326 Sequence 2326, App
129 7 1.2 11 7 US-11-045-024-2328 Sequence 2328, App
130 7 1.2 11 7 US-11-045-024-4784 Sequence 4784, App
131 7 1.2 11 7 US-11-045-024-5399 Sequence 5399, App
132 7 1.2 11 7 US-11-045-024-9643 Sequence 9643, App
133 7 1.2 12 6 US-10-989-226-17 Sequence 17, App1
134 7 1.2 12 7 US-11-066-967-44 Sequence 44, App1
135 7 1.2 15 6 US-10-431-638-6 Sequence 6, App1
136 7 1.2 15 6 US-10-513-465-6 Sequence 6, App1
137 7 1.2 15 7 US-11-045-024-13266 Sequence 13266, A
138 7 1.2 16 7 US-11-045-024-13428 Sequence 13428, A
139 7 1.2 16 7 US-11-197-488-21 Sequence 21, App1
140 7 1.2 17 6 US-10-967-457-34 Sequence 34, App1
141 7 1.2 17 7 US-11-078-663-34 Sequence 34, App1
142 7 1.2 17 7 US-11-078-914-34 Sequence 34, App1
143 7 1.2 17 7 US-11-033-039-896 Sequence 896, App
144 7 1.2 17 7 US-11-221-849-6 Sequence 6, App1
145 7 1.2 17 7 US-11-175-690-7 Sequence 7, App1
146 7 1.2 18 6 US-10-498-665-79 Sequence 79, App1
147 7 1.2 18 6 US-10-498-665-81 Sequence 81, App1
148 7 1.2 19 6 US-10-503-575-205 Sequence 205, App
149 7 1.2 20 6 US-10-623-155-553 Sequence 553, App
150 7 1.2 20 6 US-10-623-155-554 Sequence 554, App

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ALIGNMENTS

```

RESULT 1
US-10-467-657-4066
; Sequence 4066, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

```

```

; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4066
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4066

```

```

Query Match 1.8%; Score 9; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 12 LLAVALLLL 20
Db 165 LLAVALLLL 173

```

```

RESULT 2
US-10-878-556A-115
; Sequence 115, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878, 556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: sw_hum/cg11_human
; DATABASE ENTRY DATE: 2003-02-28
US-10-878-556A-115

```

```

Query Match 1.8%; Score 9; DB 6; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 131 YGHLDVQPA 139
Db 97 YGHLDVQPA 105

```

```

RESULT 3
US-11-087-099-5884
; Sequence 5884, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087, 099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5884
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Yarrowia lipolytica
US-11-087-099-5884

```

```

Query Match 1.8%; Score 9; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 12 LLAVALLLL 20
Db 349 LLAVALLLL 357

```

```

RESULT 4
US-11-123-896-278
; Sequence 278, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensein Polynucleotides and Methods of
; FILE REFERENCE: 35716/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-11-123-896-278

```

```

Query Match      1.6%; Score 8; DB 7; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      14 AVALLLLL 21
Db      10 AVALLLLL 17

```

```

RESULT 5
US-11-123-896-56
; Sequence 56, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensein Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-11-123-896-56

```

```

Query Match      1.6%; Score 8; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      14 AVALLLLL 21
Db      12 AVALLLLL 19

```

```

RESULT 6
US-11-087-099-8542
; Sequence 8542, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8542
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-087-099-8542

```

```

Query Match      1.6%; Score 8; DB 7; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      12 LAVALLLL 19
Db      11 LAVALLLL 18

```

```

RESULT 7
US-11-087-099-2900
; Sequence 2900, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2900
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-087-099-2900

```

```

Query Match      1.6%; Score 8; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      12 LAVALLLL 19
Db      13 LAVALLLL 20

```

```

RESULT 8
US-11-140-416-34
; Sequence 34, Application US/11140416
; Publication No. US20060029547A1
; GENERAL INFORMATION:
; APPLICANT: D-Gen Limited
; TITLE OF INVENTION: BIOLOGICAL MATERIALS AND METHODS USEFUL IN THE
; FILE REFERENCE: ICOT/P21952
; CURRENT APPLICATION NUMBER: US/11/140,416
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: GB 9624091.4
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34

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LENGTH: 277
TYPE: PRT
ORGANISM: Gallus gallus
US-11-140-416-34

Query Match
Best Local Similarity 100.0%; Score 8; DB 7; Length 277;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LAVLLLLL 20
Db 263 LAVLLLLL 270

RESULT 9
US-11-096-568A-12504
Sequence 12504, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12504
LENGTH: 293
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(293)
OTHER INFORMATION: Ceres Seq. ID no. 14301931
US-11-096-568A-12504

Query Match
Best Local Similarity 100.0%; Score 8; DB 7; Length 293;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 SSSPPPPA 34
Db 97 SSSPPPPA 104

RESULT 10
US-11-037-243-100
Sequence 100, Application US/11037243
Publication No. US20050287546A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHITE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDASANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/11/037,243
CURRENT FILING DATE: 2005-05-26
PRIOR APPLICATION NUMBER: US/09/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100
LENGTH: 578
TYPE: PRT
ORGANISM: Homo sapiens
US-11-037-243-100

Query Match 1.6%; Score 8; DB 7; Length 578;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLAVLLLL 19
Db 2 LLAVLLLL 9

RESULT 11
US-11-096-568A-20038
Sequence 20038, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20038
LENGTH: 579
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(579)
OTHER INFORMATION: Ceres Seq. ID no. 12376563
US-11-096-568A-20038

Query Match
Best Local Similarity 100.0%; Score 8; DB 7; Length 579;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LAVLLLLL 20
Db 17 LAVLLLLL 24

RESULT 12
US-10-645-441-15
Sequence 15, Application US/10645441
Publication No. US20050260599A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Ryba, Nicholas J.P.
APPLICANT: Nelson, Greg
APPLICANT: Hoon, Mark A.
APPLICANT: Chandrasekar, Jayaram
APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Mammalian Sweet Taste Receptors
FILE REFERENCE: 02307E-120110US
CURRENT APPLICATION NUMBER: US/10/645,441
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: US/09/927,315
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/302,898
PRIOR FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 852
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human T1R3 sweet taste receptor
US-10-645-441-15

Query Match 1.6%; Score 8; DB 6; Length 852;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
Db 568 AVLLLLLL 575

RESULT 13

US-10-725-475-7
Sequence 7, Application US/10725475
Publication No. US20060014208A1

GENERAL INFORMATION:
APPLICANT: ZOLLER, MARK
APPLICANT: LI, XIAODONG
APPLICANT: STASZEWSKI, LENA
APPLICANT: O'CONNELL, SHAWN
APPLICANT: KOZULYA, SERGEY
APPLICANT: ADLER, JON
APPLICANT: XU, HONG
APPLICANT: ECHEVERRI, FERNANDO
TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
FILE REFERENCE: 078003-0291566
CURRENT APPLICATION NUMBER: US/10/725,475
CURRENT FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: 60/300,434
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/304,749
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/310,493
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/331,771
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/339,472
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/372,090
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/374,143
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7
LENGTH: 852
TYPE: PRT
ORGANISM: Homo sapiens
US-10-725-475-7

Query Match 1.6%; Score 8; DB 6; Length 852;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
Db 568 AVLLLLLL 575

RESULT 14
US-11-050-804-6
Sequence 6, Application US/11050804
Publication No. US20050287517A1

GENERAL INFORMATION:
APPLICANT: ADLER, JON ELLIOT
APPLICANT: LI, XIAODONG
APPLICANT: STASZEWSKI, LENA
APPLICANT: XU, HONG
APPLICANT: ECHEVERRI, FERNANDO
TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
FILE REFERENCE: T1530-00006
CURRENT APPLICATION NUMBER: US/11/050,804
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: 09/897,427

PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/284,547
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 60/300,434
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 6
LENGTH: 852
TYPE: PRT
ORGANISM: Homo sapiens
US-11-050-804-6

Qy 14 AVLLLLLL 21
Db 568 AVLLLLLL 575

Query Match 1.6%; Score 8; DB 7; Length 852;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
Db 568 AVLLLLLL 575

RESULT 15
US-11-113-424-36
Sequence 36, Application US/11113424
Publication No. US20050260713A1

GENERAL INFORMATION:
APPLICANT: Gangoli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/307,506
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/322,358
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/294,075
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/288,153
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 999
TYPE: PRT
ORGANISM: Homo sapiens
US-11-113-424-36

Query Match 1.6%; Score 8; DB 7; Length 999;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
Db 14 AVLLLLLL 21

RESULT 16
US-10-517-696-137
Sequence 137, Application US/10517696
Publication No. US20060051759A1
GENERAL INFORMATION:
APPLICANT: diadexus, Inc.

```

; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PR
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-517-696-137
```

```

Query Match          1.4%; Score 7; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      16 LLLLLL 22
        |||||
Db       3 LLLLLL 9
```

```

RESULT 17
US-11-123-896-468
; Sequence 468, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McOutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; PRIOR FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 468
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Zea mays
US-11-123-896-468
```

```

Query Match          1.4%; Score 7; DB 7; Length 79;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 AVLLLL 20
        |||||
Db       13 AVLLLL 19
```

```

RESULT 18
US-10-475-075-175
; Sequence 175, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejani, Stephane
```

```

; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jober, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 175
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18...-1
US-10-475-075-175
```

```

Query Match          1.4%; Score 7; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 VLLLLL 21
        |||||
Db       6 VLLLLL 12
```

```

RESULT 19
US-10-475-075-460
; Sequence 460, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejani, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jober, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 460
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18...-1
US-10-475-075-460
```

```

Query Match          1.4%; Score 7; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 VLLLLL 21
        |||||
Db       6 VLLLLL 12
```

```

RESULT 20
US-11-096-568A-13143
; Sequence 13143, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides I
```

```

; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13143
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(86)
; OTHER INFORMATION: Ceres Seq. ID no. 15172623
US-11-096-568A-13143

Query Match          1.4%; Score 7; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          12 LNAVLL 18
Db          11 LNAVLL 17

RESULT 21
US-11-176-951-11
; Sequence 11, Application US/11176951
; Publication No. US2006002431A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, YUAN-SHOU
; APPLICANT: CHEN, XIN
; TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF
; FILE REFERENCE: 08642.0019
; CURRENT APPLICATION NUMBER: US/11/176,951
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 60/586,095
; PRIOR FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: 60/585,952
; PRIOR FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 11
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-951-11

Query Match          1.4%; Score 7; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          201 EAGSVAL 207
Db          18 EAGSVAL 24

RESULT 22
US-10-485-788A-775
; Sequence 775, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rablnowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03

```

```

; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 775
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-775

Query Match          1.4%; Score 7; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          303 LTEEBIN 309
Db          2 LTEEBIN 8

RESULT 23
US-11-053-076-157
; Sequence 157, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-157

Query Match          1.4%; Score 7; DB 7; Length 101;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          303 LTEEBIN 309
Db          2 LTEEBIN 8

RESULT 24

```

```
US-10-475-075-242
; Sequence 242, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Benjamin, Hiroaki
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 242
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16...-1
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.61791418904325
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 84
; OTHER INFORMATION: Xaa = Phe or Tyr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa = Gln or His
; US-10-475-075-242

Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 129;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 14 AVLLLLL 20
Db 2 AVLLLLL 8

RESULT 25
US-10-475-075-243
; Sequence 243, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 243
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16...-1
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.61791418904325
; OTHER INFORMATION: score 3.61791418904325
```

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; OTHER INFORMATION: seq LLLLRALRRGPG/PG
US-10-475-075-243

Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 129;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 14 AVLLLLL 20
Db 2 AVLLLLL 8

RESULT 26
US-10-475-075-513
; Sequence 513, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 513
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16...-1
; US-10-475-075-513

Query Match
Best Local Similarity 100.0%; Score 7; DB 6; Length 129;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 14 AVLLLLL 20
Db 2 AVLLLLL 8

RESULT 27
US-10-644-807-297
; Sequence 297, Application US/10644807
; Publication No. US20060057582A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: P5735
; CURRENT APPLICATION NUMBER: US/10/644,807
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: PCT/US02/05064
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,658
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/304,444
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 445
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 297
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (34)
```



```

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (69)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (96)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-644-807-297

```

```

Query Match
Best Local Similarity 1.4%; Score 7; DB 6; Length 133;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 15 VLAVLL 21
Db 26 VLAVLL 32

```

```

RESULT 28
US-11-096-568A-13303
Sequence 13303, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 13303
LENGTH: 154
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(154)
OTHER INFORMATION: Cereas Seq. ID no. 15174286
US-11-096-568A-13303

```

```

Query Match
Best Local Similarity 1.4%; Score 7; DB 7; Length 154;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 27 SSPSP 33
Db 132 SSPSP 138

```

```

RESULT 29
US-11-096-568A-22510
Sequence 22510, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22510
LENGTH: 160
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature

```

```

LOCATION: (1)..(160)
OTHER INFORMATION: Cereas Seq. ID no. 12409034
US-11-096-568A-22510

```

```

Query Match
Best Local Similarity 1.4%; Score 7; DB 7; Length 160;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 15 VLAVLL 21
Db 35 VLAVLL 41

```

```

RESULT 30
US-10-467-657-2842
Sequence 2842, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan9, version 1.04
SEQ ID NO 2842
LENGTH: 161
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2842

```

```

Query Match
Best Local Similarity 1.4%; Score 7; DB 6; Length 161;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 13 LAVVLL 19
Db 95 LAVVLL 101

```

```

Search completed: March 30, 2006, 09:16:46
Job time : 24 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 30, 2006, 09:08:07 ; Search time 40 Seconds
(without alignments)
1221.953 Million cell updates/sec

Title: US-10-849-979-139

Perfect score: 508

Sequence: 1 MDPKLGMAASLAVLLLL.....NYIEGTLPAFPLEMAQLH 508

Scoring table: OLIGO

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3510

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.0	379	2 AB1108	succinyl-diaminopim
2	10	2.0	481	2 SS6289	hypothetical prote
3	9	1.8	177	2 D83727	RNA polymerase ECF
4	9	1.8	248	2 B81096	CDPdiacylglycerol-
5	9	1.8	369	2 C69256	succinyl-diaminop
6	9	1.8	400	2 B72650	hypothetical prote
7	9	1.8	473	2 T24197	hypothetical prote
8	9	1.8	497	2 S43745	phosphatidylinosit
9	9	1.8	841	2 S74280	hypothetical prote
10	8	1.6	82	2 JC7897	defensin 1 precurs
11	8	1.6	154	2 A05187	hypothetical prote
12	8	1.6	267	1 UJCH	major prion protei
13	8	1.6	267	2 A37372	prion protein homo
14	8	1.6	273	2 A46280	prion protein - ch
15	8	1.6	317	2 AF0792	conserved hypothet
16	8	1.6	325	2 T05166	quinone reductase
17	8	1.6	336	2 T45730	peroxidase-like pr
18	8	1.6	364	1 SAVLD	large surface anti
19	8	1.6	365	1 SAVLM	conserved hypothet
20	8	1.6	372	2 T42426	succinyl-diaminop
21	8	1.6	377	2 B82846	leukostatin precu
22	8	1.6	378	2 S00842	hypothetical prote
23	8	1.6	412	2 F87460	hypothetical prote
24	8	1.6	423	2 B83106	lipoprotein - Stre
25	8	1.6	451	2 S78104	C4-dicarboxylate t
26	8	1.6	463	2 D75262	hypothetical prote
27	8	1.6	522	2 T18657	probable chemotaxi
28	8	1.6	545	2 F83280	fibropellin C prec
29	8	1.6	570	2 A48836	

30	8	1.6	645	2 T19382	hypothetical prote
31	8	1.6	837	2 AB1383	hypothetical membr
32	8	1.6	880	2 D89756	protein T35E7.2b (
33	8	1.6	931	2 H96527	protein F27015.16
34	8	1.6	1002	1 GNLJND	HIV-1 retrovirus
35	7	1.4	86	2 A35241	198 Fc receptor ga
36	7	1.4	91	2 C97909	hypothetical prote
37	7	1.4	91	2 G91275	hypothetical prote
38	7	1.4	91	2 G86116	hypothetical prote
39	7	1.4	91	2 S56424	hypothetical prote
40	7	1.4	97	2 C70828	hypothetical prote
41	7	1.4	99	2 S09522	nodC protein - Rhl
42	7	1.4	107	2 T35523	probable small sec
43	7	1.4	133	2 S57038	probable membrane
44	7	1.4	135	2 AH3610	hypothetical membr
45	7	1.4	135	2 AG2045	hypothetical prote
46	7	1.4	147	2 A53180	ribonuclease PL3 (
47	7	1.4	152	2 D75367	hypothetical prote
48	7	1.4	156	2 B83138	hypothetical prote
49	7	1.4	159	2 B84669	hypothetical prote
50	7	1.4	161	2 D81940	probable membrane
51	7	1.4	161	2 B81166	hypothetical prote
52	7	1.4	168	2 B83975	hypothetical prote
53	7	1.4	169	2 B48458	surface antigen -
54	7	1.4	171	2 S19502	hypothetical prote
55	7	1.4	172	2 A49652	caltractin - human
56	7	1.4	172	2 T38424	caltractin - human
57	7	1.4	172	2 S38531	caltractin - mouse
58	7	1.4	172	2 A39458	carotene biosynthe
59	7	1.4	174	2 S30200	ribosomal protein
60	7	1.4	179	2 S01400	H+-transporting tw
61	7	1.4	179	2 AH2528	hypothetical prote
62	7	1.4	182	2 AE1857	ribosome recycling
63	7	1.4	185	2 A49957	CD45-associated 30
64	7	1.4	190	2 F72207	probable ribosomal
65	7	1.4	194	2 A72727	conserved hypothet
66	7	1.4	194	2 B82492	membrane protein L
67	7	1.4	197	2 S51372	hypothetical prote
68	7	1.4	199	2 T45543	splicing factor RS
69	7	1.4	200	2 T52627	splicing factor 9G
70	7	1.4	200	2 D75154	hypothetical prote
71	7	1.4	204	2 T05112	pathogenesis relat
72	7	1.4	205	2 T48294	lymphocyte phospha
73	7	1.4	206	2 A55412	Ig lambda-5 chain
74	7	1.4	209	1 A26166	hrp protein - Pse
75	7	1.4	209	2 S61856	diagnalyte cyclas
76	7	1.4	212	2 AB3591	conserved hypothet
77	7	1.4	221	2 F87428	recombination acti
78	7	1.4	221	2 JCA761	probable protein-L
79	7	1.4	223	2 B95367	H+-transporting tw
80	7	1.4	227	2 T11825	oxotidine 5' monop
81	7	1.4	231	1 S74852	pseudouridylylate sy
82	7	1.4	231	2 AG0785	hypothetical 25.9
83	7	1.4	231	2 F64987	16S pseudouridylyl
84	7	1.4	231	2 B85857	16S pseudouridylyl
85	7	1.4	231	2 C91013	probable periplasm
86	7	1.4	234	2 AB1871	conserved hypothet
87	7	1.4	241	2 C81028	transcription regu
88	7	1.4	241	2 AF3327	myelin P0 protein
89	7	1.4	247	1 A54662	myelin P0 protein
90	7	1.4	247	1 JH0252	myelin P0 protein
91	7	1.4	248	1 MPRTO	myelin P0 protein
92	7	1.4	251	2 T38053	myelin protein zer
93	7	1.4	253	2 A97052	probable lytic mur
94	7	1.4	261	2 AD2747	hypothetical prote
95	7	1.4	261	2 C97528	antigenic protein
96	7	1.4	263	2 S57346	interleukin 15 rec
97	7	1.4	271	2 A48826	low choriolytic ha
98	7	1.4	271	2 S38046	hypothetical prote
99	7	1.4	272	1 S28795	carbonate dehydrat
100	7	1.4	272	2 B83610	sulfate transport
101	7	1.4	272	2 F87269	hypothetical prote
102	7	1.4	274	2 A71140	hypothetical prote

103	7	1.4	275	2	A32410	tryptase (EC 3.4.2
104	7	1.4	284	2	S58650	hypothetical prote
105	7	1.4	287	1	S75686	suppressor protein
106	7	1.4	292	2	D71181	hypothetical prote
107	7	1.4	294	2	T34048	hypothetical prote
108	7	1.4	295	2	A12981	ABC transporter, m
109	7	1.4	295	2	G96301	hypothetical ABC t
110	7	1.4	295	2	AE1663	transcription acti
111	7	1.4	296	2	G72760	hypothetical prote
112	7	1.4	301	2	S51439	hypothetical prote
113	7	1.4	305	2	E95622	hypothetical prote
114	7	1.4	308	2	AE2960	hypothetical prote
115	7	1.4	319	2	A96323	ABC transporter, p
116	7	1.4	319	2	S62196	hypothetical prote
117	7	1.4	323	2	T05478	peroxidase (EC 1.1
118	7	1.4	331	2	A85430	peroxidase like pr
119	7	1.4	336	2	H84767	probable peroxidase
120	7	1.4	339	2	T37487	hypothetical prote
121	7	1.4	342	2	A90894	probable transport
122	7	1.4	342	2	H85723	probable transport
123	7	1.4	351	2	S20078	NOV protein - chic
124	7	1.4	355	2	D71429	hypothetical prote
125	7	1.4	359	2	S39605	class I histocompa
126	7	1.4	359	2	PQ0468	chreonine ammonia-
127	7	1.4	365	2	S64466	cathepsin B (EC 3.
128	7	1.4	365	2	B42832	factor VIII introm
129	7	1.4	366	1	SAVLBD	large surface anti
130	7	1.4	366	1	SAVLMD	large surface anti
131	7	1.4	368	2	A41111	flagellum-associat
132	7	1.4	377	2	F97267	uncharacterized co
133	7	1.4	378	2	S14959	proline-rich prote
134	7	1.4	378	2	AB1469	succinyl-diaminopim
135	7	1.4	380	2	A42832	factor VIII-associ
136	7	1.4	381	2	S48049	cholecystokinin B
137	7	1.4	383	2	T21453	hypothetical prote
138	7	1.4	386	2	C81256	probable 2,3,4,5-c
139	7	1.4	389	2	G70810	probable transcrip
140	7	1.4	396	2	B64306	hypothetical prote
141	7	1.4	397	2	T00098	hypothetical prote
142	7	1.4	398	2	S66465	cathepsin B (EC 3.
143	7	1.4	398	2	C90349	multidrug-efflux t
144	7	1.4	401	2	F68834	multidrug-efflux t
145	7	1.4	405	2	AE0534	P2B/LAMP-1 precurs
146	7	1.4	407	2	E89991	hypothetical prote
147	7	1.4	410	2	JC7584	basic helix-loop-h
148	7	1.4	415	2	G85066	hypothetical prote
149	7	1.4	420	2	I51667	thrombin receptor
150	7	1.4	429	2	AD2939	hypothetical prote

ALIGNMENTS

RESULT 1
 succinyl-diaminopimelate desuccinylase homolog [imported] - *Listeria monocytogenes*
 C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AB1108
 R:Glaeser, P.; Frangoul, L.; Buchtiseer, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsthl, H.; D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schueter, T.; Simoes, N.; Tlerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlard, A.; Title: Comparative genomics of *Listeria* species
 A:Reference number: AB1077; MUID:21537279; PMID:11679665
 A:Accession: AB1108
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-379 <GLA>
 A:Cross-references: UNIPROT:Q9ZEYO; UNIPARC:UPI0000054F38; GB:NC_003210; PIDN:CAD00792.1
 A:Experimental source: strain EGD-e

C:Genetics:
 A:Gene: lmo0265
 C:Superfamily: Succinyl-diaminopimelate desuccinylase

Query Match 2.0%; Score 10; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKLYGRGATD 166
 DB 94 GKLYGRGATD 103

RESULT 2

S56239
 hypothetical protein YFR044c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein F06
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 05-Oct-2004
 C:Accession: S56239; S62255; S63791

R:Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, S.I.; Title: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces cerevisiae*
 A:Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces cerevisiae*
 A:Reference number: S56186
 A:Accession: S56239
 A:Molecule type: DNA
 A:Residues: 1-481 <MUR>

A:Cross-references: UNIPROT:P43616; UNIPARC:UPI0000052F2D; EMBL:D50617; NID:G836685; PID R:Murakami, Y.
 Submitted to the EMBL Data Library, December 1994
 A:Reference number: S62250
 A:Accession: S62255
 A:Molecule type: DNA
 A:Residues: 1-481 <MUR>

A:Cross-references: UNIPARC:UPI0000052F2D; EMBL:D44597; NID:G871938; PIDN:BA08010.1; PIR R:Kikuchi, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.
 Yeast 12, 149-167, 1996
 A:Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI
 A:Reference number: S63787; MUID:96287652; PMID:866379

A:Accession: S63791
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-481 <EKT>
 A:Cross-references: UNIPARC:UPI0000052F2D; EMBL:D44597; NID:G871938; PIDN:BA08010.1; PIR R:Kikuchi, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.
 Yeast 12, 149-167, 1996
 A:Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI
 A:Reference number: S63787; MUID:96287652; PMID:866379

A:Accession: S63791
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-481 <EKT>
 A:Cross-references: UNIPARC:UPI0000052F2D; EMBL:D44597; NID:G871938; PIDN:BA08010.1; PIR R:Kikuchi, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.
 Yeast 12, 149-167, 1996
 A:Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI
 A:Reference number: S63787; MUID:96287652; PMID:866379

A:Accession: S63791
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-481 <EKT>
 A:Cross-references: UNIPARC:UPI0000052F2D; EMBL:D44597; NID:G871938; PIDN:BA08010.1; PIR R:Kikuchi, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.
 Yeast 12, 149-167, 1996
 A:Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI
 A:Reference number: S63787; MUID:96287652; PMID:866379

QY 343 WRYSLSITNG 352
 DB 314 WRYSLSITNG 323

RESULT 3

DB3727
 RNA polymerase ECF-type sigma factor sigV [imported] - *Bacillus halodurans* (strain C-125)
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: DB3727

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and its
 A:Reference number: AB3650; MUID:20515582; PMID:11058132
 A:Accession: DB3727
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-379 <GLA>
 A:Cross-references: UNIPROT:Q9ZEYO; UNIPARC:UPI0000054F38; GB:NC_003210; PIDN:CAD00792.1
 A:Experimental source: strain EGD-e

A/Residues: 1-177 <STO>
A/Cross-references: UNIPROT:Q9K66; UNIPARC:UPI00000C392E; GB:AP001509; GB:BA000004; NID
A/Experimental source: strain C-125
C/Genetics:
A/Gene: slgV

Query Match 1.8%; Score 9; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 208 BELVEKED 216
DB 17 BELVEKED 25

RESULT 4
E81096
CDP-diacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8) NMA1532 [imported] - Nei
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: E81096; G81844
R/Retelion: H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, V.; Gill, V.; Scariato, V.; Maignani, V.; Pizsa, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: E81096
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-248 <TE>
A/Cross-references: UNIPROT:Q9UR61; UNIPARC:UPI00000C4E16; GB:AE002480; GB:AE002098; NID
A/Experimental source: serogroup B, strain MC58
R/Berkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R.; Holtz, S.; Vogelz, K.; Leach, S.; Mout, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: G81844
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-248 <PAR>
A/Cross-references: UNIPARC:UPI00000C4E16; GB:AL162756; GB:AL157959; NID:G7380091; PIDN:
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: pgs; NMA1318; NMA1532
C/Superfamily: CDP-diacylglycerol-serine O-phosphatidyltransferase; Bacillus subtilis C
C/Keywords: transferase
F/42-192/Domain: Bacillus subtilis CDP-diacylglycerol-serine O-phosphatidyltransferase hc

Query Match 1.8%; Score 9; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 LLAVALLL 20
DB 204 LLAVALLL 212

RESULT 5
C69256
succinyl-diaminopimelate desuccinylase (dapE-1) homolog - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C/Accession: C69256
R/Klem, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.P.
Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Ueberbach, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A/Reference number: A69250; MUID:98049343; PMID:9389475
A/Accession: C69256
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-369 <KLE>
A/Cross-references: UNIPROT:Q30185; UNIPARC:UPI0000057267; GB:AE001103; GB:AE000782; NID
C/Superfamily: Succinyl-diaminopimelate desuccinylase

Query Match 1.8%; Score 9; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 VDGKLYGRG 163
DB 82 VDGKLYGRG 90

RESULT 6
B72650
hypothetical protein APE0632 - Aeropyrum pernix (strain KL)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C/Accession: B72650
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ka
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310359; PMID:10382966
A/Accession: B72650
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <KAW>
A/Cross-references: UNIPROT:Q9YER4; UNIPARC:UPI000005DC0F; DDBJ:AP000060; NID:G5104188; I
A/Experimental source: strain KL
C/Genetics:
A/Gene: APE0632
C/Superfamily: Succinyl-diaminopimelate desuccinylase

Query Match 1.8%; Score 9; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 156 DGKLYGRGA 164
DB 98 DGKLYGRGA 106

RESULT 7
T24197
hypothetical protein R11H6.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C/Accession: T24197
R/Bardill, S.
submitted to the EMBL Data Library, March 1997
A/Reference number: Z19852
A/Accession: T24197
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-473 <WIL>
A/Cross-references: UNIPROT:O18000; UNIPARC:UPI0000080893; EMBL:Z93386; PIDN:CAM07646.1;
A/Experimental source: clone R11H6
C/Genetics:
A/Gene: C8SP; R11H6.1
A/Map position: 5
A/Introns: 101/1; 261/1
C/Superfamily: Peptidase V

Query Match 1.8%; Score 9; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 YGHLDVQPA 139

RESULT 12

UTCH

major prion protein homolog precursor - chicken

C/Species: Gallus gallus (chicken)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: A41280; B41280

R/Harris, D.A.; Faller, D.L.; Johnson, F.A.; Fischbach, G.D.

Proc. Natl. Acad. Sci. U.S.A. 88, 7664-7668, 1991

A/Title: A prion-like protein from chicken brain copurifies with an acetylcholine receptor

A/Reference number: A41280; PMID:91352049; PMID:1715573

A/Accession: A41280

A/Molecule type: mRNA

A/Residues: 1-267 <HAR>

A/Cross-references: UNIPROT:P27177; UNIPARC:UPI0000171396; GB:M61145; NID:G212614; PIDN:

A/Experimental source: day-18 brain

A/Accession: B41280

A/Molecule type: protein

A/Residues: 25-51 <HA2>

A/Cross-references: UNIPARC:UPI0000174093

A/Note: the protein was purified from adult chicken brain on the basis of its ability to

C/Comment: Enzymatic release studies show that this protein has a glycosylphosphatidylin

C/Superfamily: major prion protein

C/Keywords: brain; glycoprotein; phosphatidylinositol linkage; prion; scrapie

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-267/Product: major prion protein homolog #status predicted <MAT>

F/188,203,212/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match

Best Local Similarity 1.6%; Score 8; DB 1; Length 267;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 LAVALLL 20

253 LAVALLL 260

RESULT 13

A37372

prion protein homolog precursor - chicken

C/Species: Gallus gallus (chicken)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 07-May-1999

C/Accession: A37372

R/Faller, D.L.; Harris, D.A.; Johnson, F.A.; Morgan, M.M.; Corfas, G.; Fischbach, G.D.

Cold Spring Harb. Symp. Quant. Biol. 55, 397-406, 1990

A/Title: M-r 42,000 ARIA: a protein that may regulate the accumulation of acetylcholine

A/Reference number: A37372; PMID:92111159; PMID:2132829

A/Accession: A37372

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: mRNA

A/Residues: 1-267 <PAL>

A/Cross-references: UNIPARC:UPI000017777A; GB:M61145

C/Superfamily: major prion protein

Query Match

Best Local Similarity 1.6%; Score 8; DB 2; Length 267;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 LAVALLL 20

253 LAVALLL 260

RESULT 14

A46280

prion protein - chicken

C/Species: Gallus gallus (chicken)

C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A46280

R/Gabriel, J.M.; Oesch, B.; Kretzschmar, H.; Scott, M.; Prusiner, S.B.

Proc. Natl. Acad. Sci. U.S.A. 89, 9097-9101, 1992

A/Title: Molecular cloning of a candidate chicken prion protein.

A/Reference number: A46280; PMID:93028411; PMID:1409608

A/Accession: A46280

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-273 <GAB>

A/Cross-references: UNIPROT:P27177; UNIPARC:UPI0000132205; GB:M95404; NID:G212610; PIDN:

A/Note: sequence extracted from NCBI backbone (NCBIN:115392, NCBIPI:115393)

C/Superfamily: major prion protein

Query Match

Best Local Similarity 1.6%; Score 8; DB 2; Length 273;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 LAVALLL 20

259 LAVALLL 266

RESULT 15

AF0792

conserved hypothetical protein STY2517 [imported] - Salmonella enterica subsp. enterica

C/Species: Salmonella enterica subsp. enterica serovar typh

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AF0792

R/Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Mout, S.; O'Garra, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; PMID:21534947; PMID:11677608

A/Accession: AF0792

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-317 <PAR>

A/Cross-references: UNIPARC:UPI00000CB87; GB:AL513382; PIDN:CAD07520.1; PID:G1503513; C

C/Genetics:

A/Gene: STY2517

Query Match

Best Local Similarity 1.6%; Score 8; DB 2; Length 317;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 326 RVEKFLFD 333

37 RVEKFLFD 44

RESULT 16

T05166

guanine reductase homolog F18B5.200 - Arabidopsis thaliana

N/Alternate names: hypothetical protein F17L22.40

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T05166; T05833

R/Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Newe

submitted to the Protein Sequence Database, February 1998

A/Reference number: Z15400

A/Accession: T05166

A/Molecule type: DNA

A/Residues: 1-325 <BEV>

A/Cross-references: UNIPROT:O65423; UNIPARC:UPI000009F5A5; EMBL:AL022603

A/Experimental source: cultivar Columbia; BAC clone F18B5

R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bar

submitted to the Protein Sequence Database, February 1999

A/Accession: T05833

A/Molecule type: DNA

A/Residues: 1-325 <BEV>

A/Cross-references: UNIPARC:UPI000009F5A5; EMBL:AL035527

A/Experimental source: cultivar Columbia; BAC clone F17L22

C/Genetics:

A/Map position: 4

A:introns: 84/3; 144/3; 172/1; 261/1
 A:Note: P1885.200; P17122.40
 C:superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 1.6%; Score 8; DB 2; Length 325;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 ADTLORLG 90
 DB 42 ADTLORLG 49

RESULT 17

T45730
 peroxidase-like protein - Arabidopsis thaliana

N:contains: major surface antigen; middle surface antigen

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T45730

R:Yitale, D.; Liguori, R.; Flores, M.; Argiriu, A.; De Simone, V.; Nemes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23012

A:Accession: T45730

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-336 <YIT>

A:Cross-references: UNIPROT:Q9SD46; UNIPARC:UPI00004882D; EMBL:AL132980

A:Experimental source: cultivar Columbia; BAC clone F24M12

C:Genetics:

A:Map position: 3

A:introns: 78/3; 142/3; 198/1

A:Note: P24M12.30

C:superfamily: peroxidase

Query Match 1.6%; Score 8; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 DLVALIGS 283
 DB 192 DLVALIGS 199

RESULT 18

SAVLD
 large surface antigen - duck hepatitis virus

N:contains: major surface antigen; middle surface antigen

C:Species: duck hepatitis virus, DHBV

C:Date: 20-Sep-1984 #sequence_revision 20-Sep-1984 #text_change 31-Dec-2004

C:Accession: A03710; S12845

R:Mandart, E.; Kay, A.; Galibert, F.

J. Virol. 49; 782-792, 1984

A:Title: Nucleotide sequence of a cloned duck hepatitis B virus genome: comparison with

A:Reference number: A93997; MUID:84138772; PMID:6699938

A:Accession: A03710

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-364 <MAN>

A:Cross-references: UNIPROT:Q92935; UNIPARC:UPI0000174975; GB:X01834

R:Matres, F.; Tong, S.; Teubner, K.; Blum, H.E.

Nucleic Acids Res. 18; 6140, 1990

A:Title: Complete nucleotide sequence of a German duck hepatitis B virus.

A:Reference number: S12843; MUID:91045092; PMID:2235507

A:Accession: S12845

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 36-364 <MAT>

A:Cross-references: UNIPARC:UPI000009AFA; EMBL:X12798

C:Genetics:

A:Gene: pre-S1/pre-S2/S

C:Keywords: glycoprotein; surface antigen

F:89-364/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>

F:198-364/Product: major surface antigen (gene S) #status predicted <MSA>

F:32,170,296/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.6%; Score 8; DB 1; Length 364;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 SGTFGGIL 270
 DB 199 SGTFGGIL 206

RESULT 19

SAVIME

large surface antigen - duck hepatitis virus (strain China)

N:contains: major surface antigen; middle surface antigen

C:Species: duck hepatitis virus, DHBV

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: S12842

R:Tong, S.; Matres, F.; Teubner, K.; Blum, H.E.

Nucleic Acids Res. 18; 6139, 1990

A:Title: Complete nucleotide sequence of a Chinese duck hepatitis B virus.

A:Reference number: S12840; MUID:91045091; PMID:2235506

A:Accession: S12842

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-365 <TON>

A:Cross-references: UNIPROT:P30029; UNIPARC:UPI00001389B2; GB:M21953; NID:G325435; PIDN:J

C:Genetics:

A:Gene: pre-S1/pre-S2/S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: glycoprotein; surface antigen

F:89-365/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>

F:199-365/Product: major surface antigen (gene S) #status predicted <MSA>

F:297/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.6%; Score 8; DB 1; Length 365;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 SGTFGGIL 270
 DB 200 SGTFGGIL 207

RESULT 20
 T42426
 conserved hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004

C:Accession: T42426

R:Yoshida, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.

DNA Res. 4; 363-369, 1997

A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A:Reference number: Z17323; MUID:98162722; PMID:9501991

A:Accession: T42426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-372 <YOS>

A:Cross-references: UNIPROT:P78801; UNIPARC:UPI000006C66C; EMBL:D89150; NID:G1749507; PII

A:Experimental source: strain FR745

C:Superfamily: Peptidase V

Query Match 1.6%; Score 8; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 VIGKFSIR 377
 DB 268 VIGKFSIR 275

RESULT 21

B82846

succiny1-diaminopimelate desucciny1ase XP0116 [imported] - Xylella fastidiosa (strain 94
 C/Species: Xylella fastidiosa
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
 C/Accession: B82846
 R/Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A/Reference number: A82515; PMID:20365717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: B82846
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-377 <STM>
 A/Cross-references: UNIPROT:Q9PH30; UNIPARC:UPI00000C22DE; GB:AE003865; GB:AE003849; NID
 A/Experimental source: strain 945C
 R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H
 de-Neto, E.; Docena, C.; El-Dorcy, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A/Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laig
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A/Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A/Reference number: A59328
 A/Content: annotation
 C/Genetics:
 A/Genes: XP0116
 C/Superfamily: Succiny1-diaminopimelate desucciny1ase

Query Match 1.6%; Score 8; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKLYGRGA 164
 |||||
 DB 90 GKLYGRGA 97

RESULT 22
 S00842
 leukostalin precursor - rat (fragment)
 N/Alternate names: leucocyte statoglycoprotein; statophorin
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: S00842
 R/Killien, N.; Barclay, A.N.; Willis, A.C.; Williams, A.F.
 EMBO J. 6, 4029-4034, 1987
 A/Title: The sequence of rat leukostalin (W/13 antigen) reveals a molecule with O-link
 A/Reference number: S00842; MUID:816646; PMID:2965006
 A/Accession: S00842
 A/Molecule type: mRNA
 A/Residues: 1-378 <KIL>
 A/Cross-references: UNIPROT:P13838; UNIPARC:UPI00001255AB; EMBL.Y00090; NID:956573; PIN
 C/Superfamily: leukostalin
 C/Keywords: glycoprotein; transmembrane protein
 P/1-7/Domain: signal sequence #status predicted <SIG>
 P/8-3/8/Product: leukostalin #status predicted <MAT>

Query Match 1.6%; Score 8; DB 2; Length 378;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 GSVALLEL 210
 |||||
 DB 329 GSVALLEL 336

RESULT 23
 P87460

hypothetical protein CC1706 [imported] - Caulobacter crescentus
 C/Species: Caulobacter crescentus
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C/Accession: F87460
 R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 J.; Leub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of Caulobacter crescentus.
 A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: F87460
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-412 <STO>
 A/Cross-references: UNIPROT:Q9A7L6; UNIPARC:UPI00000C7493; GB:AE005673; NID:G13423120; P
 C/Genetics:
 A/Genes: CC1706

Query Match 1.6%; Score 8; DB 2; Length 412;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AVLLLLLL 21
 |||||
 DB 6 AVLLLLLL 13

RESULT 24
 B83106
 hypothetical protein PA4321 [imported] - Pseudomonas aeruginosa (strain PA01)
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: B83106
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brf
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lilm,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: B83106
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-423 <STO>
 A/Cross-references: UNIPROT:Q9H80; UNIPARC:UPI00000C5CB9; GB:AE004848; GB:AE004091; NID:
 A/Experimental source: strain PA01
 C/Genetics:
 A/Genes: PA4321

Query Match 1.6%; Score 8; DB 2; Length 423;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLAVLLLL 19
 |||||
 DB 10 LLAVLLLL 17

RESULT 25
 S78104
 lipoprotein - Streptomyces antibioticus
 C/Species: Streptomyces antibioticus
 C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jul-2004
 C/Accession: S78104; S33183
 R/Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.
 Submitted to the EMBL Data Library, September 1993
 A/Description: Characterization of a Streptomyces antibioticus gene cluster encoding a g
 A/Reference number: S78104
 A/Accession: S78104
 A/Molecule type: DNA
 A/Residues: 1-451 <HER>
 A/Cross-references: UNIPROT:Q53684; UNIPARC:UPI000013BC70; EMBL.Z22577; NID:G404284; PID
 A/Experimental source: strain ATCC 11891
 A/Note: this is a revision to the sequence from reference S33182

R.Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.
submitted to the EMBL Data Library, April 1993
A.Description: Characterization of a Streptomyces antibiotic gene cluster encoding a g
A.Reference number: S33182
A.Accession: S33183
A.Molecule type: DNA
A.Residues: 1-422, 'LPALTR', 423-430, 'AY', 433, 'AOE', 437, 'EIVE', 444, 'Q', 446-447, 'VYRRRRDHPT
A.Cross-References: UNIPARC:UPI000017AD90; EMBL:Z22577
A.Experimental source: strain ATCC 11891
A.Note: this sequence has been revised in reference S78104

Query Match 1.6%; Score 8; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAAVLLLL 20
|||||
Db 9 LAAVLLLL 16

RESULT 26

D75262
C4-dicarboxylate transport protein - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Accession: D75262
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.U.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Usterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Reference number: A75250; MUID:20036896; PMID:10567266
A.Accession: D75262
A.Molecule type: DNA
A.Status: preliminary
A.Residues: 1-463 <WHI>
A.Cross-References: UNIPARC:UPI0000164CCF; GB:AE002082; GB:AE000513; NID:g6460347; PIDN:
A.Experimental source: strain R1
A.Genetics:
A.Gene: DR2525
A.Map position: 1
C.Superfamily: C4-dicarboxylate carrier protein

Query Match 1.6%; Score 8; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 SLAAVLLL 18
|||||
Db 350 SLAAVLLL 357

RESULT 27

T18657
hypothetical protein B0035.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T18657
R.White, S.
submitted to the EMBL Data Library, May 1996
A.Reference number: Z19002
A.Accession: T18657
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-522 <WIL>
A.Cross-References: UNIPROT:Q27464; UNIPARC:UPI000012AF14; EMBL:Z73102; PIDN:CAA97412.1;
A.Experimental source: clone B0035
A.Genetics:
A.Gene: CESP:B0035.5
A.Map position: 4
A.Introns: 42/3, 111/3, 137/1, 221/2, 322/1, 368/1, 435/2, 494/2
C.Superfamily: glucose-6-phosphate dehydrogenase

Query Match 1.6%; Score 8; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 LPVNIKFI 195
|||||
Db 63 LPVNIKFI 70

RESULT 28

F83280
Probable chemotaxis transducer PA2920 (imported) - Pseudomonas aeruginosa (strain PA01)
C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C.Accession: F83280
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A.Reference number: A82950; MUID:20437337; PMID:10984043
A.Accession: F83280
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-545 <STO>
A.Cross-References: UNIPROT:Q9H2S7; UNIPARC:UPI00000C5883; GB:AE004718; GB:AE004091; NID:
A.Experimental source: strain PA01
A.Genetics:
A.Gene: PA2920

Query Match 1.6%; Score 8; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LAAVLLLL 19
|||||
Db 20 LAAVLLLL 27

RESULT 29

A48836
fibropellin C precursor - sea urchin (Strongylocentrotus purpuratus)
N.Alternate names: EGF repeat-containing protein; epidermal growth factor-related protei
C.Species: Strongylocentrotus purpuratus (purple urchin)
C.Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A48836
R.Bisgrove, B.W.; Raff, R.A.
Dev. Biol. 157, 526-538, 1993
A.Title: The SPEGF III gene encodes a member of the fibropellins: EGF repeat-containing f
A.Reference number: A48836; MUID:93273088; PMID:8500658
A.Accession: A48836
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-570 <BIS>
A.Cross-References: UNIPROT:P49013; UNIPARC:UPI000012A573; GB:L07045; NID:g310659; PID:g
A.Note: sequence extracted from NCBI backbone (NCBIN:132724, NCBI:P:132725)
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-570/Product: fibropellin C #status predicted <PIB>
F:19-54/Domain: EGF homology <EG1>
F:57-175/Domain: C1r/C1s repeat homology <C1R>
F:176-211/Domain: EGF homology <EG2>
F:214-249/Domain: EGF homology <EG3>
F:252-287/Domain: EGF homology <EG4>
F:290-325/Domain: EGF homology <EG5>
F:328-363/Domain: EGF homology <EG6>
F:366-401/Domain: EGF homology <EG7>
F:404-439/Domain: EGF homology <EG8>
F:442-570/Region: avidin-like
F:23-34,28-43,45-54,62-86,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-276
Iide bonds: #status predicted

Query Match 1.6%; Score 8; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 28;

	Matches	8;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	11									
Db	4	SLAVLL	11							

RESULT 30
T19382
hypothetical protein C18D1.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T19382
R/Berks, M.
submitted to the EMBL Data Library, March 1995
A/Reference number: Z19117
A/Accession: T19382
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-645 <Wild>
A/Cross-references: UNIPROT:Q09478; UNIPARC:UPI000008359C; EMBL:Z48543; PIDN:CAA88432.1;
A/Experimental source: clone C18D1
C/Genetic8:
A/Gene: CBSP:C18D1.1
A/Map position: 2
A/Intons: 16/3; 133/3; 296/3; 574/3; 611/1

Query Match 1.6%; Score 8; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 SSPSPPA 34
|||||
Db 144 SSPSPPA 151

Search completed: March 30, 2006, 09:12:35
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: March 30, 2006, 09:04:47 ; Search time 233 Seconds
(without alignments)
1538.233 Million cell updates/sec

Title: US-10-849-979-139

Perfect score: 508

Sequence: 1 MPEKLGKRMASLIVALLLL.....NYIEGKLFAPAFLEMAQLH 508

Scoring table: OLIGO

Searched: 2166443 seqs, 705528306 residues

Word size : 6

Total number of hits satisfying chosen parameters: 34363

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	407	80.1	508	1	CPGL2_HUMAN
2	148	29.1	171	2	Q6ZND4_HUMAN
3	145	28.5	464	2	Q5RA69_PONPY
4	32	6.3	482	2	Q80XP5_MOUSE
5	32	6.3	482	2	Q8BUG2_MOUSE
6	30	5.9	492	2	Q6HGG3_RAT
7	15	3.0	357	2	Q81IB0_DROWI
8	15	3.0	471	2	Q81IU9_DROVI
9	15	3.0	478	2	Q6C1A8_YARLI
10	15	3.0	478	2	Q4WMD5_ASPTU
11	15	3.0	489	2	Q8ANF8_XENLA
12	15	3.0	494	2	Q7ZXAG_XENLA
13	15	3.0	500	2	Q801E4_XENLA
14	13	2.6	494	2	Q6PA54_XENLA
15	11	2.2	184	2	Q7ZUZ2_OREMO
16	11	2.2	407	2	Q4RUC4_TERTG
17	11	2.2	474	2	Q6DH98_BRARE
18	11	2.2	474	2	Q6DUK5_XENLA
19	11	2.2	474	2	Q6P358_XENTR
20	11	2.2	474	2	Q6TNAV3_BRARE
21	11	2.2	474	2	Q7TOR7_XENLA
22	11	2.2	475	2	Q5ZLV5_CHICK
23	11	2.2	477	2	Q5B7M1_EMENT
24	11	2.2	478	2	Q5V9H1_DROME
25	10	2.0	26	2	Q9ESQ6_MOUSE
26	10	2.0	156	2	Q6QMP8_LISMO
27	10	2.0	157	2	Q6QMP6_LISMO
28	10	2.0	157	2	Q6QMP0_LISMO
29	10	2.0	159	2	Q83UD0_LISMO
30	10	2.0	159	2	Q84GK9_LISMO
31	10	2.0	351	2	Q8T213_METWA

32	10	2.0	379	2	Q9EXF4_LISMO	Q9EXF4 listeria mo
33	10	2.0	379	2	Q9ZEY0_LISMO	Q9ZEY0 listeria mo
34	10	2.0	455	2	Q4SUU3_TERTG	Q4SUU3 tetraodon n
35	10	2.0	476	2	Q4HYR5_GIBZE	Q4HYR5 gibberella
36	10	2.0	481	1	CPGL_YEAST	CPGL_YEAST
37	10	2.0	483	2	Q6FWY0_CANGA	Q6FWY0 candida gla
38	10	2.0	501	1	PTGIS_MOUSE	PTGIS mus musculu
39	10	2.0	509	2	PTGIS_RAT	PTGIS rattus norv
40	10	2.0	509	2	Q8BXC0_MOUSE	Q8BXC0 mus musculu
41	10	2.0	533	2	Q6CYE6_KULIA	Q6CYE6 kluyveromyc
42	10	2.0	607	2	Q5W239_MAIZE	Q5W239 zea mays (m
43	10	2.0	1030	2	Q4ITX0_AZOVI	Q4ITX0 azotobacter
44	9	1.8	99	2	Q4TEH3_TERTG	Q4TEH3 tetraodon n
45	9	1.8	100	2	Q9LDG6_ORISA	Q9LDG6 oryza sativ
46	9	1.8	103	2	Q4YXS4_HUMAN	Q4YXS4 homo sapien
47	9	1.8	170	2	Q9NUV1_HUMAN	Q9NUV1 homo sapien
48	9	1.8	173	2	Q6XHG1_DROYA	Q6XHG1 drosophila
49	9	1.8	177	2	Q9KRF6_BACHD	Q9KRF6 bacillus ha
50	9	1.8	194	2	Q6UX25_HUMAN	Q6UX25 homo sapien
51	9	1.8	194	2	Q4YXS6_HUMAN	Q4YXS6 homo sapien
52	9	1.8	209	2	Q8NDY8_HUMAN	Q8NDY8 homo sapien
53	9	1.8	225	2	Q84ZC8_ORISA	Q84ZC8 oryza sativ
54	9	1.8	248	2	Q5F920_NEIGI	Q5F920 neisseria g
55	9	1.8	248	2	Q9JRF61_NEIMA	Q9JRF61 neisseria m
56	9	1.8	248	2	Q7DDC6_NEIMB	Q7DDC6 neisseria m
57	9	1.8	252	2	Q7P3P6_FUSUN	Q7P3P6 fusobacteri
58	9	1.8	276	2	Q9H7K8_HUMAN	Q9H7K8 homo sapien
59	9	1.8	311	2	Q9NM02_HUMAN	Q9NM02 homo sapien
60	9	1.8	369	2	Q30185_ARCFU	Q30185 archaeoglob
61	9	1.8	378	2	Q82292_ENTFA	Q82292 enterococcu
62	9	1.8	379	2	Q4LN79_9BURA	Q4LN79 burkholderi
63	9	1.8	379	2	Q62JBI_BURMA	Q62JBI burkholderi
64	9	1.8	383	2	Q63T00_BURPS	Q63T00 burkholderi
65	9	1.8	386	2	Q8XK55_RALSO	Q8XK55 ralsstonia s
66	9	1.8	391	2	Q8WY59_HUMAN	Q8WY59 homo sapien
67	9	1.8	400	2	Q9YEB4_AERPE	Q9YEB4 aeropyrum p
68	9	1.8	401	2	Q6KAT3_MOUSE	Q6KAT3 mus musculu
69	9	1.8	403	2	Q5W2P6_LEGSL	Q5W2P6 legionella
70	9	1.8	406	2	Q89T45_BRATA	Q89T45 bradyrhizob
71	9	1.8	411	2	Q8KMB1_PSEAE	Q8KMB1 pseudomonas
72	9	1.8	411	2	Q9XC62_PSEAE	Q9XC62 pseudomonas
73	9	1.8	418	2	Q67UY9_ORISA	Q67UY9 oryza sativ
74	9	1.8	443	2	Q9BL46_CABEL	Q9BL46 caenorhabdi
75	9	1.8	471	2	Q61JDD3_CABER	Q61JDD3 caenorhabdi
76	9	1.8	473	2	Q61W41_CABER	Q61W41 caenorhabdi
77	9	1.8	475	1	Q18000_CABEL	Q18000 caenorhabdi
78	9	1.8	475	1	CPGL1_HUMAN	CPGL1 homo sapien
79	9	1.8	475	1	CPGL1_MOUSE	CPGL1 mus musculu
80	9	1.8	475	2	Q5R432_PONPY	Q5R432 pongo pygma
81	9	1.8	475	2	Q5R510_PONPY	Q5R510 pongo pygma
82	9	1.8	475	2	Q6QDN1_RAT	Q6QDN1 rattus norv
83	9	1.8	476	2	Q560T2_CRYNE	Q560T2 cryptococcu
84	9	1.8	476	2	Q5KPT1_CRYNE	Q5KPT1 cryptococcu
85	9	1.8	477	2	Q4PCK5_USITMA	Q4PCK5 usitlago ma
86	9	1.8	477	2	Q7OJ09_ANOGA	Q7OJ09 anopheles g
87	9	1.8	499	2	Q6P336_XENTR	Q6P336 xenopus tro
88	9	1.8	512	2	Q8RG48_FUSNN	Q8RG48 fusobacteri
89	9	1.8	519	2	Q7NIC7_GLOVI	Q7NIC7 gloeobacter
90	9	1.8	790	2	Q53U95_MAIZE	Q53U95 zea mays (m
91	9	1.8	832	2	Q413K7_GIBZE	Q413K7 gibberella
92	9	1.8	841	1	SPB1_YEAST	SPB1 saccharomyc
93	9	1.8	896	2	Q4NY52_9DELT	Q4NY52 anaeromyxob
94	9	1.8	947	2	Q4FVY0_TETMA	Q4FVY0 tetrahymena
95	9	1.8	947	2	Q4NS17_9DELT	Q4NS17 anaeromyxob
96	8	1.6	53	2	Q6H8C6_ORISA	Q6H8C6 oryza sativ
97	8	1.6	82	2	Q6R529_ORENI	Q6R529 oreochromis
98	8	1.6	86	2	Q6R529_ORENI	Q6R529 oreochromis
99	8	1.6	110	2	Q5JAN3_ORISA	Q5JAN3 oryza sativ
100	8	1.6	111	2	Q6R528_ORENI	Q6R528 oreochromis
101	8	1.6	114	1	NPRF_RAT	NPRF rattus norv
102	8	1.6	115	2	Q6UXD1_HUMAN	Q6UXD1 homo sapien
103	8	1.6	115	2	Q7U487_SYNPX	Q7U487 synechococc
104	8	1.6	115	2	Q6R530_ORENI	Q6R530 oreochromis

105	8	1.6	118	2	Q8BHM3_MOUSE	Q8bhm3 m mus muscu
106	8	1.6	146	1	LSH6_MACRO	Q46483 macrocrus ru
107	8	1.6	138	2	Q61ID7_DROME	Q61id7 drosophila
108	8	1.6	165	2	Q91XF7_9H1V1	Q91xf7 human immu
109	8	1.6	166	2	Q8BJE9_PSBPK	Q8bj9 pseudomon
110	8	1.6	167	2	Q4LL26_9BURK	Q4ll26 burkholderi
111	8	1.6	167	2	Q6QUC5_HPBUD	Q6quc5 duck hepati
112	8	1.6	167	2	Q6RSF0_HPBUD	Q6rsf0 duck hepati
113	8	1.6	167	2	Q6RSF5_HPBUD	Q6rsf5 duck hepati
114	8	1.6	167	2	Q9WFA7_9HEPA	Q9wfa7 snow goose
115	8	1.6	167	2	Q9WFB0_9HEPA	Q9wfb0 snow goose
116	8	1.6	167	2	Q9WFB4_9HEPA	Q9wfb4 snow goose
117	8	1.6	167	2	Q9WFB7_9HEPA	Q9wfb7 snow goose
118	8	1.6	167	2	Q89689_HPBUD	Q89689 duck hepati
119	8	1.6	170	1	DEP1_BORBR	Q7w9g bordetella
120	8	1.6	170	1	DEP1_BORPA	Q7wv3 bordetella
121	8	1.6	170	1	DEP2_BORPE	Q7v88 bordetella
122	8	1.6	174	2	Q76WH1_9TELE	Q76wh1 saccopharyn
123	8	1.6	180	2	Q6IKJ8_DROME	Q6ikj8 drosophila
124	8	1.6	183	2	Q6Z1A0_ORYSA	Q6z1a0 oryza sativ
125	8	1.6	192	2	Q64FU1_HORSE	Q64fu1 equus cabal
126	8	1.6	204	2	Q7SSY2_ECOLI	Q7s5y2 escherichia
127	8	1.6	206	1	RL25_THET2	Q72a7 thermus the
128	8	1.6	206	1	RL25_THET8	Q5ehz1 thermus the
129	8	1.6	206	1	RL25_THET9	P56j30 thermus the
130	8	1.6	208	2	Q5KRW6_GEOXA	Q5kzw6 geobacillus
131	8	1.6	209	2	Q9SS31_ARATH	Q9ss31 arabidopsis
132	8	1.6	210	2	Q7SSX6_ECOLI	Q7s5x6 escherichia
133	8	1.6	211	2	Q74MG5_NANEO	Q74mg5 nanorchaeu
134	8	1.6	234	2	Q7SGL3_ORYSA	Q7s5l3 oryza sativ
135	8	1.6	237	2	Q9WGS2_9H1V1	Q9wgs2 human immu
136	8	1.6	237	2	Q9WGV8_9H1V1	Q9wgv8 human immu
137	8	1.6	237	2	Q9WGW0_9H1V1	Q9wgw0 human immu
138	8	1.6	237	2	Q9WGM1_9H1V1	Q9wgm1 human immu
139	8	1.6	238	2	Q67MD8_ORYSA	Q67md8 oryza sativ
140	8	1.6	243	2	Q7PVG3_ANGOA	Q7pvg3 anopheles g
141	8	1.6	248	2	Q8I275_PROVU	Q8i275 proteus vul
142	8	1.6	262	1	UPPP1_METKA	P58887 mechanopyru
143	8	1.6	270	1	UPPP1_BACCI	P62461 bacillus ce
144	8	1.6	270	1	UPPP2_BACCR	Q8ltv4 bacillus ce
145	8	1.6	270	1	UPPP2_BACCR	Q6ltw2 bacillus ce
146	8	1.6	270	1	UPPP2_BACCH	Q6hnd2 bacillus th
147	8	1.6	270	1	UPPP3_BACCH	Q8lvt1 bacillus an
148	8	1.6	270	1	Q4MLJ0_BACCE	Q4mlj0 bacillus ce
149	8	1.6	273	1	PRI0_CHICK	P27177 gallus gall
150	8	1.6	273	2	Q6JMI3_MERUD	Q6jmi3 melospittac

ALIGNMENTS

RESULT 1
CPGL2_HUMAN STANDARD; PRT; 508 AA.
AC Q96KQ2; Q6UWK2; Q9BTP8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glutamate carboxypeptidase-like protein 2 precursor (CNDP dipeptidase 1).
GN Name=CNDP1, Synonyms=CPGL2, ORFNames=UNQ1915/PRO4380;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Chen J.M., Barrett A.J.;
RT "Cloning and sequencing of a second human homologue of glutamate carboxypeptidase in peptidase family M20,";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=2288796; PubMed=12975309; DOI=10.1101/gr.1293003;
RX CLARK H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Sestagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Watnabe C., Wiand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 199-508.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rabe S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Roark S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez P., Prange C.,
RA Whitting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the peptidase M20A family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ417564; CAD10388.1; -; mRNA.
DR EMBL; AY358756; AA089116.1; -; mRNA.
DR EMBL; BC004271; -; NOT_ANNOTATED_CDS; mRNA.
DR MERRIPS; M20.006; -; NOT_ANNOTATED_CDS; mRNA.
DR Eneemb; ENSG00000150656; Homo sapiens.
DR HGNC; HGNC:20675; CNDP1.
DR MIM; 609064; -.
DR InterPro; IPR001261; ARG_E_dape.
DR InterPro; IPR011650; M20_dimer.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF07687; M20_dimer; 1.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00758; ARG_E_DAPE_CPG2_1; FALSE_NEG.
DR PROSITE; PS00759; ARG_E_DAPE_CPG2_2; 1.
KW Carboxypeptidase; Hydrolase; Metalloprotease; Protease; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 508 Glutamate carboxypeptidase-like protein
FT FT
FT FT
FT CONFLICT 21 21 Missing (in Ref. 2).
FT CONFLICT 156 156 G -> D (in Ref. 2).
FT CONFLICT 238 238 P -> L (in Ref. 1).
FT CONFLICT 273 273 P -> L (in Ref. 1).
SQ SEQUENCE 508 AA; 56747 MW; 8B9EAL5FA277553E CRC64;

Query Match 80.1%; Score 407; DB 1; Length 508;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPKLGMAASLAVLLILLERGMFSSPPPLLEKVFQYIDLHODEFVQTLKEKVAI 60
 DB 1 MDPKLGMAASLAVLLILLERGMFSSPPPLLEKVFQYIDLHODEFVQTLKEKVAI 60

QY 61 ESDSVQVPRPRROELFRMVAADTLORIGARVSVSMGPQQLPDDGSLPPPIITAEIG 120
 DB 61 ESDSVQVPRPRROELFRMVAADTLORIGARVSVSMGPQQLPDDGSLPPPIITAEIG 120

QY 121 SDPTKGTVCFFGHLDVOPADRGDMLTDPYVLTEDVKLXGRGATDKKGPYLAMINAVSA 180
 DB 121 SDPTKGTVCFFGHLDVOPADRGDMLTDPYVLTEDVKLXGRGATDKKGPYLAMINAVSA 180

QY 181 PRALQDLPNVNIKTIIGMEBAGSVALBELVEKEDRPFSGVDYIISDNLWISQRKPAI 240
 DB 181 PRALQDLPNVNIKTIIGMEBAGSVALBELVEKEDRPFSGVDYIISDNLWISQRKPAI 240

QY 241 TYGTRGNSYFWEVEKCRDODPFGSLIHEPMADIVALLGSLVDSGHIIVPGIYDEV 300
 DB 241 TYGTRGNSYFWEVEKCRDODPFGSLIHEPMADIVALLGSLVDSGHIIVPGIYDEV 300

QY 301 VPLTEEBINTYKAIHLDEEYRNSRYEKFLEDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
 DB 301 VPLTEEBINTYKAIHLDEEYRNSRYEKFLEDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

QY 361 GTKTVIIGRYIGKRSILVPHMNVSAVEKQVTRHLEDFSKRNSNKMVSMITGLHPWT 420
 DB 361 GTKTVIIGRYIGKRSILVPHMNVSAVEKQVTRHLEDFSKRNSNKMVSMITGLHPWT 420

QY 421 ANIDDDTOYLAKAIRVFGTEPMDIRDSSTIPAKKFOEIVKRSVYLILGLAVDGEHS 480
 DB 421 ANIDDDTOYLAKAIRVFGTEPMDIRDSSTIPAKKFOEIVKRSVYLILGLAVDGEHS 480

QY 481 QNEKINRMNYIEGKTLPAAFFLEMAQLH 508
 DB 481 QNEKINRMNYIEGKTLPAAFFLEMAQLH 508

RESULT 2
 ID Q6ZND4 HUMAN PRELIMINARY; PRT; 171 AA.
 AC Q6ZND4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein FLJ16195.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NCLEOTIDE SEQUENCE.
 RP TISSUE=Thalamus;
 RA Oca T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hito Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Megasehima M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
 RA Menubo Y., Nagai K., Isogai T.,
 RU Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL AKJ11263; BAD18441.1; -; mRNA.
 DR GO:GO:0008237; F:metallopeptidase activity; IEA.
 DR InterPro: IPR011650; M20 dimer.
 DR Pfam: PF07687; M20 dimer; 1.
 SO SEQUENCE 171 AA; 18880 MW; 20816D6D8F214688 CRC64;

Query Match 29.1%; Score 148; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3; 9e-133;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 MHLNRPISLHIEGAFDEPGTKTVIPGRVIGKESIRLVPHMNVSAVEKQVTRHLEDFV 399
 DB 1 MHLNRPISLHIEGAFDEPGTKTVIPGRVIGKESIRLVPHMNVSAVEKQVTRHLEDFV 399

QY 400 SKNNSNKMVSVSTLGLHPINIIDPTOYLAKRAIRTYGTEPMDIRDSSTIPAKKFO 459
 DB 61 SKNNSNKMVSVSTLGLHPINIIDPTOYLAKRAIRTYGTEPMDIRDSSTIPAKKFO 120

QY 460 EIVKSVVLIPLGAVDGEHSQNEKINR 487
 DB 121 EIVKSVVLIPLGAVDGEHSQNEKINR 148

RESULT 3
 ID Q5RA69 PONPY PRELIMINARY; PRT; 464 AA.
 AC Q5RA69;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Hypothetical protein DKFZp459C1929.
 GN Name=DKFZp459C1929;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Pongo.
 NCBI_TaxID=9600;
 RN NCLEOTIDE SEQUENCE.
 RP TISSUE=Cortex;
 RA The German CDNA Consortium;
 RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.,
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR859150; CAH91341.1; -; mRNA.
 DR GO:GO:0016787; F:hydrolase activity; IEA.
 DR GO:GO:0008237; F:metallopeptidase activity; IEA.
 DR GO:GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001261; ArgR_dape.
 DR InterPro: IPR011650; M20 dimer.
 DR InterPro: IPR002933; Peptidase_M20.
 DR Pfam: PF07687; M20 dimer; 1.
 DR Pfam: PF01546; Peptidase_M20; 1.
 DR PROSITE: PS00759; ARG_E_DAP_Cp62_2; 1.
 KW Hypothetical protein.
 SO SEQUENCE 464 AA; 51970 MW; 7AAS5EAF536B0FF3C CRC64;

Query Match 28.5%; Score 145; DB 2; Length 464;
 Best Local Similarity 100.0%; Pred. No. 7; 2e-130;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 GOSLPIPVITLAEISDPTKGTVCFFGHLDVOPADRGDMLTDPYVLTEDVKLXGRGAT 165
 DB 62 GOSLPIPVITLAEISDPTKGTVCFFGHLDVOPADRGDMLTDPYVLTEDVKLXGRGAT 121

QY 166 DNKGPYLAMINAVSAFRALEQDLPNVNIKTIIGMEBAGSVALBELVEKEDRPFSGVDYI 225
 DB 122 DNKGPYLAMINAVSAFRALEQDLPNVNIKTIIGMEBAGSVALBELVEKEDRPFSGVDYI 181

QY 226 VISDNLMWISQRKPAITVGTGRNSYF 250
 DB 182 VISDNLMWISQRKPAITVGTGRNSYF 206

RESULT 4
 ID Q80XP5 MOUSE PRELIMINARY; PRT; 492 AA.
 AC Q80XP5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Carnosine dipeptidase 1 (Metallopeptidase M20 family).
 GN Name=Cndp1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schaller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stepelco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.D., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marx M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RA Strauberg R.;
 RU Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC043305; AA043305.1; -; mRNA.
 DR MEROPS; M20.006; -.
 DR MGI; MGI:2451097; Cndp1.
 DR GO; GO:0016787; Phospholipase activity; IEA.
 DR GO; GO:0008237; Phospholipase activity; IEA.
 DR GO; GO:0006508; Proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001261; ArgE_dome.
 DR InterPro; IPR011650; M20_dimer.
 DR InterPro; IPR002933; Peptidase_M20.
 DR Pfam; PF07687; M20_dimer; 1.
 DR Pfam; PF01546; Peptidase_M20; 1.
 DR PROSITE; PS00759; ARG_E_DOME; CPG2.2; 1.
 SQ SEQUENCE 492 AA; 55056 MW; 8F5C3AFD859EC04 CRC64;
 Query Match 6.3%; Score 32; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 2,3e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 339 LMHLWRYPSLSIHGEGADEGCTVITGRV 370
 DB 313 LMHLWRYPSLSIHGEGADEGCTVITGRV 344
 RESULT 5
 Q8BU02_MOUSE PRELIMINARY; PRT; 492 AA.
 ID Q8BU02_MOUSE PRELIMINARY;
 AC Q8BU02;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
 DE library, clone: D630009N02 product: similar to GLUTAMATE
 DE CARBOXYPEPTIDASE-LIKE PROTEIN 2.
 DE Name=Cndp1; Synonyms=Cn1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischiemann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guestinich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wyszewski B., Yoshida K., Hasegawa Y., Kawai H., Kontsevskii S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.153600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsui S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kaga I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Koda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK085308; BAC93417.1; -; mRNA.
 DR MEMOS: M20.006; -;
 DR Ensembl: ENSMUSG0000056162; Mus musculus.
 DR MG1: MG1.2451097; Cntrl.
 DR GO: GO:0004180; F:carboxypeptidase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0008227; F:metallopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR01261; ARG_dape.
 DR InterPro: IPR01650; M20_dimer.
 DR InterPro: IPR02933; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20; 1.
 DR PROSITE: PS00759; ARG_DAPE_CPG2_2; 1.
 DR Carboxypeptidase.
 KM SEQUENCE 492 AA; 55090 MW; 5A3E3F984CBF4567 CRC64;
 SQ

Query Match 5.3%; Score 32; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 2.3e-21;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 339 LMHMRYPSTSHIGEGAFDEPGTKTVIPGRV 370
 |||||
 Db 313 LMHMRYPSTSHIGEGAFDEPGTKTVIPGRV 344

RESULT 6
 Q66HG3 RAT PRELIMINARY; PRT; 492 AA.
 ID Q66HG3 RAT
 AC Q66HG3 RAT
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to carnosinase 1.
 GN Name=MGC93742;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RC TISSUE=Kidney;
 RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner R.H., Shennan C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tothiyuki S., Cantucci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Medan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;

RA Director MGC Project;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC081877; AA81877.1; -; mRNA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0008227; F:metallopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR01261; ARG_dape.
 DR InterPro: IPR01650; M20_dimer.
 DR InterPro: IPR02933; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20; 1.
 DR PROSITE: PS00759; ARG_DAPE_CPG2_2; 1.
 DR SEQUENCE 492 AA; 54927 MW; EF8DAE8C15BF06F5 CRC64;
 SQ

Query Match 5.9%; Score 30; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 HLMRYPSTSHIGEGAFDEPGTKTVIPGRV 370
 |||||
 Db 315 HLMRYPSTSHIGEGAFDEPGTKTVIPGRV 344

RESULT 7
 Q811B0 DROVI PRELIMINARY; PRT; 357 AA.
 ID Q811B0 DROVI
 AC Q811B0 DROVI
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG17337-PA (Fragment).
 GN ORFNames=CG17337;
 OS Drosophila willistoni (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7260;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC SPRAIN=Ducson 14030-0814.10;
 RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
 RA Gaithe A., Mungall C.J., Wang A.M., Kronmiller B., Paclebo J., Park S.,
 RA Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
 RA Celniker S.E.;
 RT "Assessing the impact of comparative genomic sequence data on the
 functional annotation of the Drosophila genome."
 RL Genome Biol. 3:research0086-research0086(2002).
 DR EMBL: AY190950; AA001061.1; -; Genomic_DNA.
 DR FLYBase: FBgn0064294; Dwl\CG17337.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0008237; F:metallopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR01261; ARG_dape.
 DR InterPro: IPR01650; M20_dimer.
 DR InterPro: IPR02933; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20; 1.
 DR Pfam: PF01546; Peptidase_M20; 1.
 DR PROSITE: PS00759; ARG_DAPE_CPG2_2; 1.
 DR NON_TER 357
 FT SEQUENCE 357 AA; 39775 MW; 2016BB8876040141 CRC64;
 SQ

Query Match 3.0%; Score 15; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 WRYPSTSHIGEGAF 357
 |||||
 Db 316 WRYPSTSHIGEGAF 330

RESULT 8
 Q811J9 DROVI PRELIMINARY; PRT; 471 AA.
 ID Q811J9 DROVI

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AC 081129;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE CG17337.
GN ORFNames=CG17337;
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydraidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoekling R.A.,
RA Gritke A., Mungall C.J., Wang A.M., Krommiller B., Pacleb J., Park S.,
RA Scapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA Celniker S.E.;
RT "Assessing the impact of comparative genomic sequence data on the
RT functional annotation of the Drosophila genome."
RL Genome Biol. 3:research0086-research0086(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pfeiffer B.D., Bergman C.M., George R.A., Mungall C.J., Pacleb J.,
RA Park S., Wan K.M., Rubin G.M., Celniker S.E.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY186999; AAN87275.1; -; Genomic_DNA.
DR FlyBase; FBgn0064314; Dvir|CG17337.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgE_DABE.
DR InterPro; IPR011650; M20_dimer.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF07687; M20_dimer; 1.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00759; ARG_E_DABE_CPG2_2; 1.
SQ SEQUENCE 471 AA; 52672 MW; 16837C27B556D9AD CRC64;

Query Match 3.0%; Score 15; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 343 WRYPSLSTHGIGAF 357
DB 307 WRYPSLSTHGIGAF 321

RESULT 9
OC1A8 YARLI PRELIMINARY; PRT; 478 AA.
AC 06C1A8_
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Yarrowia lipolytica chromosome F of strain C1899 of Yarrowia
DE lipolytica.
GN OrderedContigNames=YAL10F17842g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Pubmed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,
RA Goffard N., Frangul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Blayksten C.,
RA Boissarie A., Boyer J., Catolico L., Contalieri F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropfi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire I., Ma L., Muller H.,
RA Niclaud J.-M., Nikoljki M., Oztas S., Ozier-Kalogeropoulos O.,
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RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof B., Mitch B.,
RA Zentou-Meyer M., Zivanovic Y., Bolotin-Pukhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliardin C., Weissenbach J.,
RA Wincker P., Souciet J.-.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
DR EMBL; CR382132; CAG78363.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgE_dapr.
DR InterPro; IPR011650; M20_dimer.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF07687; M20_dimer; 1.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00759; ARG_E_DABE_CPG2_2; 1.
KW Complete proteome.
SQ SEQUENCE 478 AA; 52510 MW; 995D0F33F5FCD2A CRC64;

Query Match 3.0%; Score 15; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 343 WRYPSLSTHGIGAF 357
DB 311 WRYPSLSTHGIGAF 325

RESULT 10
OQWMD5 ASPFU
ID OQWMD5 ASPFU PRELIMINARY; PRT; 478 AA.
AC OQWMD5_
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Glutamate carboxypeptidase, putative.
GN ORFNames=Afu305450.
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley J.,
RA Artzy J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foekker N., Fraser A., Garcia J.L., Garcia M.J., Gobie A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gilliam R., Haas B.,
RA Haas H., Harris D., Horthuch H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouli H., Kitamoto K., Kobayashi T., Kulikarni R.,
RA Kumagai T., Lafont A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinolwisch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Drenth D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF01000002; EAL93018.1; -; Genomic_DNA.
DR Carboxypeptidase.
KW SEQUENCE 478 AA; 53015 MW; 62481C384B095CDB CRC64;
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DE Glutamate carboxypeptidase-like protein 1 (Fragment).
 OS Oecochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes; Labroidae;
 OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiaini;
 OC Oecochromis.
 RN NCBI_TaxId=8127;
 RP NUCLEOTIDE SEQUENCE.
 RA LO M.J., Chan L.W., Weng C.F.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY260749; AAP22042.1; -; mRNA.
 DR MEROPE; M20.005; -;
 DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR011650; M20_dimer.
 DR InterPro; IPR002933; Peptidase_M20.
 DR Pfam; PF01546; Peptidase_M20; 1.
 KM Carboxypeptidase.
 FT NON_TER 1 1
 FT NON_TER 184 184
 SQ SEQUENCE 184 AA; 20271 MW; 2F2931433DA71E9A CRC64;
 Query Match 2.2%; Score 11; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 370 VIGKFSIRLVP 380
 Db 49 VIGKFSIRLVP 59
 RESULT 16
 ID Q4RLC4_TETNG PRELIMINARY; PRT; 407 AA.
 AC Q4RLC4;
 DT 13-SEP-2005 (T-EMBLrel. 31, Last Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Chromosome 21 SCAP15022, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00032549001;
 OS Tetraodon nigrovittatus (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 RN NCBI_TaxId=99883;
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bounneau L., Fischer C., Ozouf-Coetzee C., Bernot A.,
 RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dosset C., Segurens B.,
 RA Daele C., Saitanoubat M., Levy M., Boulard N., Castellano S.,
 RA Aumont C., Skalli Z., Cattolico L., Poulin J., De Bernardis V.,
 RA Cruaud C., Duprat S., Broctier P., Coutaneau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McMan P., Bosak S.,
 RA Kellis G., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigrovittatus reveals
 the early vertebrate proto-karyotype".
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.
 DR EMBL; CAAB01015022; CAG10808.1; -; Genomic_DNA.
 FT NON_TER 1 1
 SQ SEQUENCE 407 AA; 45539 MW; 4C5BBA5CECC249B4 CRC64;
 Query Match 2.2%; Score 11; DB 2; Length 407;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 370 VIGKFSIRLVP 380
 Db 269 VIGKFSIRLVP 279
 RESULT 17
 ID Q6DH98_BRAB PRELIMINARY; PRT; 474 AA.
 AC Q6DH98;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Cytosolic nonspecific dipeptidase.
 GN Name=cndp2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN NCBI_TaxId=7955;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Director MGC Project;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC076079; AAH76079.1; -; mRNA.
 DR ZFIN; ZDB-GENE-030131-5499; cndp2.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR011261; Arg_dipep.
 DR InterPro; IPR011650; M20_dimer.
 DR InterPro; IPR002933; Peptidase_M20.
 DR Pfam; PF07687; M20_dimer; 1.
 DR Pfam; PF01546; Peptidase_M20; 1.
 DR PROSITE; PS00759; ARG8_Dipep_CPG2_2; 1.
 SQ SEQUENCE 474 AA; 53212 MW; A46D0B1EBAACFB67 CRC64;
 Query Match 2.2%; Score 11; DB 2; Length 474;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q6TNV3_BRAE PRELIMINARY; PRT; 474 AA.
AC Q6TNV3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CytoSOLic nonspecific dipeptidase.
GN Name=cdp2; Synonyms=CN2;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15520368; DOI=10.1073/pnas.0407241101;
RA Song H.-D., Sun X.-J., Deng M., Zhang G.-W., Zhou Y., Wu X.-Y.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.-L., Fan H.-Y., Zou L.I.,
RA Kanxi J.P., Liu T.X., Look A.T., Chen Z.;
RT "Hematopoietic gene expression profile in zebrafish kidney marrow."
RL Proc. Natl. Acad. Sci. U.S.A. 101:16240-16245(2004).
DR EMBL: AY391414; AAC01226.1; -; mRNA.
DR ZFIN: ZDB-GENE-030131-5499; cndp2.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0008237; F:metallopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001261; ARGD_dapB.
DR InterPro: IPR002933; Peptidase_M20.
DR Pfam: PF07687; M20_dimer; 1.
DR Pfam: PF01546; Peptidase_M20; 1.
DR PROSITE: PS00759; ARGD_DAPB_CPG2_2; 1.
SQ SEQUENCE 474 AA; 53134 MW; 5147C209BD4D8AC6 CRC64;

Query Match 2.2%; Score 11; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 VIGKFSRLVP 380
Db 336 VIGKFSRLVP 346

RESULT 21
Q7TOR7_XENLA PRELIMINARY; PRT; 474 AA.
AC Q7TOR7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C12-prov protein.
GN Names=c12-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Felting E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner R.D., Shemen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohivuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Straube R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RX Submitted (MUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC056069; AAHS6069.1; -; mRNA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0008237; F:metallopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001261; ARGD_dapB.
DR InterPro: IPR011650; M20_dimer.
DR InterPro: IPR002933; Peptidase_M20.
DR Pfam: PF07687; M20_dimer; 1.
DR Pfam: PF01546; Peptidase_M20; 1.
DR PROSITE: PS00759; ARGD_DAPB_CPG2_2; 1.
SQ SEQUENCE 474 AA; 52745 MW; 33D9F60F6D375FEF CRC64;

Query Match 2.2%; Score 11; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 VIGKFSRLVP 380
Db 336 VIGKFSRLVP 346

RESULT 22
Q5ZLV5_CHICK PRELIMINARY; PRT; 475 AA.
AC Q5ZLV5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCUMB04_419;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Beznubov Y., Zaim J.,
RA Fiedler P., Kuter S., Biagiodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde U.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL: A719629; CAG31288.1; -; mRNA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0008237; F:metallopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001261; ARGD_dapB.
DR InterPro: IPR002933; Peptidase_M20.
DR Pfam: PF07687; M20_dimer; 1.

DR Pfam; PRO1546; Peptidase_M20; 1.
DR PROSITE; PS00759; ARGE_DNPE_CPG2_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 53078 MW; E7ED4945EB1D5A5 CRC64;
Query Match 2.2%; Score 11; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 370 VIGKFSRLVP 380
Db 336 VIGKFSRLVP 346
RESULT 23
Q5B7M1_EMEMI
ID Q5B7M1_EMEMI PRELIMINARY; PRT; 477 AA.
AC Q5B7M1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
DE ORFNames=AN3459.2;
GN ORFNames=AN3459.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Emericella.
OX NCBI_TaxId=227321;
RN 1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nudbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barina N., Bastien V., Bloom T., Boguslavsky L.,
RA Bouknight B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collamore A., Cook K., Cooke B., Corum B., DeArrelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gierre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hago B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Liu A.,
RA Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,
RA Mathews C., Mauceli E., McCarthy M., Mejdrit J., Menus L.,
RA Mithova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunhhang P., Piere N., Purcell S.,
RA Rachtupka A., Ramaany U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schnupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talmas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACD0100058; EAA62999.1; -; Genomic_DNA.
CC KW Hypothetical protein.
SQ SEQUENCE 477 AA; 52644 MW; 2AA6EF6E685831 CRC64;
Query Match 2.2%; Score 11; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 346 PSLSIHGIGA 356
Db 312 PSLSIHGIGA 322
RESULT 24
Q9V9H1_DROME
ID Q9V9H1_DROME PRELIMINARY; PRT; 478 AA.

AC Q9V9H1_Q6MT58; Q9V9H2; 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2004 (TrEMBLrel. 26, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG17337-PA (REL1562p).
DE ORFNames=CG17337;
GN ORFNames=CG17337;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pezomyza;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN 1)
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoeking R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jatali M.E., Kalush F., Karpen G.H., Ke Z., Kensington J.A., Ketchum K.A.,
RA Kimmel B.G., Kodali C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laevo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo K., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner T.K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimori I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaes R., Teector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodson A.,
RA George R.A., Hoeking R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaes R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RL melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaes R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomic perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).


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RN [4]
NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecousse B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.,
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
NUCLEOTIDE SEQUENCE.
RG FlyBase;
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champ M., Chavez C., Dorset V., Dresnek D., Farfan D., Frise E.,
RA Giranda R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.,
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC QV3H2:Rpn1; NBExp=1; InAct=EBI-144341, EBI-178674;
DR EMBL; AEO03785; AAF57318.2; -; Genomic_DNA.
DR EMBL; AY118368; AAM48397.1; -; mRNA.
DR InAct; QV9H1; -.
DR MEROPS; M20.005; -.
DR Ensemble; CG17337; Drosophila melanogaster.
DR FlyBase; FBgn0033035; CG17337.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0046983; F:protein dimerization activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgD_dapE.
DR InterPro; IPR002933; Peptidase_M20.
DR InterPro; IPR01546; M20_dimer.
DR Pfam; PF07687; M20_dimer; 1.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00759; ARGD_DAPE_CPG2_2; 1.
DR PROSITE; PS00759; ARGD_DAPE_CPG2_2; 1.
SQ SEQUENCE 478 AA; 53163 MW; D76738B81B7DC477 CRC64;

Query Match 2.2%; Score 11; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 VIGKFSIRLVP 380
Db 341 VIGKFSIRLVP 351

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Saurimnogoniles; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVJ; Tissue=Spleen;
RA Okawara S., Shimomishi M., Tanabe T., Yokoyama C.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040750; BAB12574.1; -; Genomic_DNA.
DR MGI; MGI:1097156; Pcg18.
DR GO; GO:0005615; C:extracellular space; TAS.
KW Cyclin.
FT NON_TER 26
SQ SEQUENCE 26 AA; 2933 MW; 7C110848736AB9E0 CRC64;

Query Match 2.0%; Score 10; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVALLLLL 21
Db 9 LVALLLLL 18

RESULT 26
Q6QMP6 LISMO
ID Q6QMP6 LISMO PRELIMINARY; PRT; 156 AA.
AC Q6QMP6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE DapE (Fragment).
GN Name=dapE;

OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Jegot G., Lanotte P., Brun S., Watt S., Quentin R., Merghetti L.,
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY533420; AAS22274.1; -; Genomic_DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgD_dapE.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00758; ARGD_DAPE_CPG2_1; UNKNOWN_1.
DR PROSITE; PS00759; ARGD_DAPE_CPG2_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 156 AA; 17042 MW; SED37075F41238E8 CRC64;

Query Match 2.0%; Score 10; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKLYRGATD 166
Db 71 GKLYRGATD 80

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RESULT 25
Q9ES06 MOUSE
ID Q9ES06 MOUSE PRELIMINARY; PRT; 26 AA.
AC Q9ES06;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Prostacyclin synthase (Fragment).
GN Name=Pcg18;

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OS  Listeria monocytogenes.
OC  Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX  NCBI_TaxID=1639;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Jegot G., Lanotte P., Brun S., Watt S., Quentin R., Mereghetti L.;
RL  Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY533422; AAS22276.1; -; Genomic DNA.
DR  GO; GO:0016787; F:hydrolase activity; IEA.
DR  GO; GO:0008237; F:metallopeptidase activity; IEA.
DR  GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR  InterPro; IPR001261; ArgE_dapE.
DR  InterPro; IPR002933; Peptidase_M20.
DR  Pfam; PF01546; Peptidase_M20; 1.
DR  PROSITE; PS00758; ARG_E_DAP_E_CPG2_1; UNKNOWN_1.
DR  PROSITE; PS00759; ARG_E_DAP_E_CPG2_2; 1.
FT  NON_TER 1 157
FT  NON_TER 1 157
SQ  SEQUENCE 157 AA; 17130 MW; 0E0DFBD2E6FE123F CRC64;

Query Match 2.0%; Score 10; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKL YGRGATD 166
DB 71 GKL YGRGATD 80

RESULT 28
ID 06OMQ0 LISMO PRELIMINARY; PRT; 157 AA.
AC 06OMQ0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE DapB (Fragment).
GN Name=dapB;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jegot G., Lanotte P., Brun S., Watt S., Quentin R., Mereghetti L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY533419; AAS22272.1; -; Genomic DNA.
DR EMBL; AY533419; AAS22273.1; -; Genomic DNA.
DR EMBL; AY533414; AAS22268.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgE_dapE.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00758; ARG_E_DAP_E_CPG2_1; UNKNOWN_1.
DR PROSITE; PS00759; ARG_E_DAP_E_CPG2_2; 1.
FT NON_TER 1 157
FT NON_TER 1 157
SQ SEQUENCE 157 AA; 17143 MW; FE1BD37075F41238 CRC64;

Query Match 2.0%; Score 10; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKL YGRGATD 166
DB 71 GKL YGRGATD 80

RESULT 29
ID 083UJ0 LISMO PRELIMINARY; PRT; 159 AA.
AC 083UJ0;

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DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Succinyldiaminopimelate desuccinylase (Fragment).
GN Name=dap;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22461922; PubMed=12574278; DOI=10.1128/JCM.41.2.757-762.2003;
RL Salcedo C., Arreaza L., Alcalá B., de la Fuente L., Vazquez J.A.;
RT "Development of a multilocus sequence typing method for analysis of
RT Listeria monocytogenes clones."
J. Clin. Microbiol. 41:757-762(2003).
DR EMBL; AY158310; AAO19550.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgE_dapE.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00758; ARG_E_DAP_E_CPG2_1; UNKNOWN_1.
DR PROSITE; PS00759; ARG_E_DAP_E_CPG2_2; 1.
FT NON_TER 1 159
FT NON_TER 1 159
SQ SEQUENCE 159 AA; 17248 MW; 44B9F7B64A9B7993 CRC64;

Query Match 2.0%; Score 10; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKL YGRGATD 166
DB 64 GKL YGRGATD 73

RESULT 30
ID 084GK9 LISMO PRELIMINARY; PRT; 159 AA.
AC 084GK9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Succinyldiaminopimelate desuccinylase (Fragment).
GN Name=dap;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22461922; PubMed=12574278; DOI=10.1128/JCM.41.2.757-762.2003;
RL Salcedo C., Arreaza L., Alcalá B., de la Fuente L., Vazquez J.A.;
RT "Development of a multilocus sequence typing method for analysis of
RT Listeria monocytogenes clones."
J. Clin. Microbiol. 41:757-762(2003).
DR EMBL; AY158310; AAO19550.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001261; ArgE_dapE.
DR InterPro; IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR PROSITE; PS00758; ARG_E_DAP_E_CPG2_1; UNKNOWN_1.
DR PROSITE; PS00759; ARG_E_DAP_E_CPG2_2; 1.
FT NON_TER 1 159
FT NON_TER 1 159
SQ SEQUENCE 159 AA; 17260 MW; 44A3DEB64A9B7993 CRC64;

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Query Match 2.0%; Score 10; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 GKLYGRGATD 166
|||
Db 64 GKLYGRGATD 73

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